

50 68.5 621 10 Q63339 MYCSIN HEAVY CHAIN 21 50 68.5 1938 10 008639 MYCSIN. 50 68.5 1972 10 008639 MYCSIN. 50 68.5 1972 10 008638 MYCSIN. 50 67.1 257 9 Q44871 PLASMID, ORFA, B, C, D 49 67.1 1983 2 015045 MYCSIN LIGHT CHAIN KIN 49 67.1 1914 2 Q15746 MYCSIN LIGHT CHAIN KIN 49 67.1 1914 2 Q15746 MYCSIN LIGHT CHAIN KIN 49 67.1 3212 3 Q94010 HYPOTHETICAL 15.4 KD P 48 65.8 164 9 P96113 POTYPETICE DEFORMYLAS 48 65.8 400 2 000328 HUWTINGTIN INTERACTING 48 65.8 401 3 Q18255 COSMID C27D9. 48 65.8 401 3 Q18255 COSMID C27D9. 48 65.8 941 2 000291 MYTOTHETICAL 119.1 KD 48 65.8 1034 3 017117 MIS1.4 PROTEIN. 48 65.8 1034 3 017117 MYTOTHETICAL 119.1 KD 48 65.8 1038 1 012532 HYPOTHETICAL 119.1 KD 48 65.8 1038 3 Q21874 ACETYL-COA CARBOXYLASE 48 65.8 2325 8 Q41743 ACETYL-COA CARBOXYLASE 48 65.8 2346 3 001385 TPR HOMOLOG. 48 65.8 2310 3 Q94658 EXPORTED SERINE/THREON	45	44	43	42	41	40	39	3 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
.5 1621 10 008639 .5 1938 10 008638 .5 1972 10 008638 .1 257 9 Q44871 .1 257 9 Q44871 .1 1991 2 Q14844 .1 1914 2 Q15045 .1 1914 2 Q15746 .1 1912 3 Q94010 .8 1133 9 P73917 .8 1040 2 Q00328 .8 481 3 Q18255 .8 481 3 Q18255 .8 943 9 Q30320 .8 943 9 Q30320 .8 1034 3 Q14527 .8 1034 3 Q15732 .8 1034 3 Q15732	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	49	49	49	49	49	49	50	50	50
10 063339 10 008638 10 008638 9 044871 1 006132 2 015045 2 015045 2 015746 3 094010 9 P73917 9 P96113 2 000328 3 018255 3 018255 3 018257 1 012527 1 012532 3 018367 1 0125367 2 014528 3 001367 3 0013685 3 0013685			•		•		•	٠	•	•	•	•	•	•	•		•	•	•		•	•	•	•	•
0 0063339 0 008638 9 008638 9 0044871 2 0046132 2 015045 2 015746 3 094010 9 P73917 9 P73917 9 P73917 9 0030320 10 0030320 10 004527 10 012532 3 018557 10 013567 10 0013867 10 0013867 10 0013867 10 0013867 10 0013867	2510	2346	2325	2024	1625	1459	1091	1038	1034	951	943	914	481	400	164	133	3212	1914	1583	991	899	257	97	93	621
8564466674007700555666	ω	w	œ	N	8	ω	ω	ب	ω	2	ဖ	N	w	N	9	9	ω	N	N	N	ᆫ	ø			
MYOSIN HEAVY CHAIN 21 MYOSIN. PLASMID, ORFA, B, C, D CHROMOSOME XII COSMID MYOSIN LIGHT CHAIN KIN KIAA0336. MYOSIN LIGHT CHAIN KIN KIAA0336. MYOSIN LIGHT CHAIN KIN OBCLII.1. HYPOTHETICAL 15.4 KD P POLYPEPTIDE DEFORMYLAS HUNTINGTIN INTERACTING COSMID C27D9. HONTINGTIN INTERACTING GOSMID C27D9. HONTINGTIN INTERACTING KIAA0291 (FRAGMENT). M151.4 PROTEIN. HYPOTHETICAL 119.1 KD SIMILARITY TO MYOSIN H R09EL0.5. ACETYL-COA CARBOXYLASE PERICENTRIOL MATERIAL ACETYL-COA CARBOXYLASE PERICENTRIOL MATERIAL ACETYL-CORNZYME A CARB TPR HOMOLOG. EXPONTED SERINE/THREON	Q94658	001385	Q41743	Q15154	Q08367	Q21874	Q18082	Q12532	_	014527	030320	000291	Q18255	000328	12	P73917	Q94010	Q15746	015045	Q14844	Q06132	Q44871	863	0863	333
	EXPORTED SERINE/THREON		A	PERICENTRIOL MATERIAL	CARBOXYLAS	Ġ	TO MYOSIN	Ļ	. 4 PR	(FRAGMENT)	ATP-DEPENDENT RNA HELI		COSMID C27D9.	INTERACTIN		15.4 KD	٠	LIGHT CHAIN		LIGHT CHAIN	IIX	D, ORFA, B, C,	MYOSIN.	MYOSIN.	HEAVY CHAIN

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RESULT OF STREET OF STREET
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Best Local (
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Q26648;
Q26648;
Q1-NOV-1996 (TREMBLREL. 01, CF
Q1-NOV-1996 (TREMBLREL. 01, L/
Q1-NOV-1996 (TREMBLREL. 01, L/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q63473;
Q63473;
Q1-NOV-1996
Q1-NOV-1996
Q1-JAN-1998
                                                                                                                                                                                                                               STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN). EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA; EUECHINOIDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94140942.
CHEN R., PERRONE C.A.,
                                                                                            SEQUENCE FROM N.A.
TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                          TEKTIN B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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|||||||||
1 LRKKLQDVHN 10
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ses 9; Conses
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(TREMBLREL: 01, LAST SEQUENCE UI
(TREMBLREL: 05, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORMONE (FRAGMENT)
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A; CHORDATA; VERTEBRATA;
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21:228-229(1984).
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         AMOS L.A., LINCK R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.
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2.77e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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DR SMEL; LAISE; 607-918(1993).

SO SPONENCE 400 AA: 46147 MN; 75400E80 CRC32;

SOET MATCHES 20 CAN: 46147 MN; 75400E80 CRC32;

SOET MATCHES 3; CONSERVATIVE 80.03; Pred. M. 2.358-600;

MATCHES 25 CONSERVATIVE 0; Mismatches 2; Indels 0; Caps 0;

JULIERIA THU JUL 30 11:11:48 1998

Job time: 29 secs.
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***	(FM)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated Thu Jul 30 10:00:59 1998; MasPar time 4.06 Seconds 83.029 Million cell updates/sec

Title:

Description: Perfect Score: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SVSEIQLM 8

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1.sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.157; Variance 18.924; scale 1.118

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query Match	Length	BG	Ħ	Description	Pred. No.
ב	50	92.6	105	10	Q63473	PARATHYROID HORMONE (F	5.43e-02
N	45	83.3	1405	10	P70366		1.44e+00
ω	45	83.3	1405	10	Q61202	STEROID RECEPTOR COACT	1.44e+00
4	45	83.3	1441	N	000150	STEROID RECEPTOR COACT	1.44e+00
տ	45	83.3	1447	10	P70365	RECEPTOR	1.44e+00
σ	44	81.5	248	9	008320	ACETYLGLUTAMATE KINASE	2.68e+00
7	43	79.6	167	9	P96578	YDAE PROTEIN.	4.96e+00
œ	43	79.6	910	11	011421	HEXON PROTEIN.	4.96e+00
9	43	79.6	911	11	Q83905	TERMINAL PROTEIN.	4.96e+00
10	42	77.8	418	ω	Q26662	VERY EARLY BLASTULA PR	9.08e+00
11	41	75.9	248	8	004682	PTI6.	1.64e+01
12	41	75.9	276	w	Q21996	SIMILAR TO TYROSINE KI	1.64e+01
13	41	75.9	373	ø	Q49979	CORA.	1.64e+01
14	41	75.9	481	\Box	Q60823	THYMOMA VIRAL PROTO-ON	1.64e+01
15	41	75.9	591		Q13026	65 KDA HYDROPHOBIC PRO	1.64e+01
16	41	75.9	591		000553	FOLATE CARRIER.	1.64e+01
17	41	75.9	896		Q55544	HYPOTHETICAL 100.3 KD	1.64e+01
18	41	75.9	1371		P73337	SENSORY TRANSDUCTION H	1.64e+01
19	41	75.9	3456	11	P89201	POLYPROTEIN.	1.64e+01
20	40	74.1	99	9	Q58911	HYPOTHETICAL 11.5 KD P	2.93e+01

3 Q19478 F15B9.1. 3 Q02074 SIMILAR TO MYC! 9 Q034472 YRI PROTEIN. 9 Q06164 SIALIDASE (FRA) 3 Q277063 SIALIDASE (FRA) 3 Q277063 SIALIDASE. 1 Q07595 RNA-DIRECTED DI 1 Q02511 HYPOTHETICAL P. 3 Q19285 F46C3.3. 1 Q19285 F46C3.3. 1 Q19285 F46C3.3. 1 Q04527 F18KOBLAST GRO! 1 Q045717 F18KOBLAST GRO! 1 Q01525 F17A2.9. 3 Q19506 F17A2.9. 3 Q1950																	29 40								
3 Q19478 F15B9.1. 3 Q19478 SIMILAR TO MY 9 Q34472 YRI PROTEIN. 9 Q06164 SIALIDASE (FR. 3 Q27063 SIALIDASE. 3 Q27064 SIALIDASE. 3 Q27995 RNA-DIRECTED 1 Q02511 HYPOTHETICAL 3 Q19285 F46C3.3. 3 Q20456 F46C3.3. 7 Q49717 B1549_F2_87. 12 Q0482 CGRP-RECEPTOR GREEN COMPANY	v	2	2	2			٠	•	•	•		•		•		•		•	74.1	74.1	74.1	74.1	74.1	74.1	74.1
019478 F1599.1. 002074 SIMILAR TO MY 034472 YRI PROTEIN. 006164 SIALIDASE (FR 227063 SIALIDASE. Q27064 SIALIDASE. Q27064 SIALIDASE. Q27064 RNA-DIRECTED Q27064 RNA-DIRECTED Q19285 HYPOTHETICAL Q19285 F46C3.3. Q20456 F46C3.3. Q20456 F46C3.3. Q20456 F46C3.3. Q20457 FIRODLAST GR Q49717 F1RODLAST GR Q90413 F1BROBLAST GR Q91742 F1BROBLAST GR Q91743 FIBROBLAST GR Q91743 FIBROBLAST GR Q91744 FIBROBLAST GR Q91745 FIBROBLAST GR Q91746 COMED FOR BY Q91746 COMED FOR BY Q91747 FIBROBLAST GR Q91748 CODED FOR BY Q91748 CODED FOR BY Q91749 CODED FOR BY Q17448 CHROMOSOME XY																									
	CHROMOSOME XVI COSMID	CODED FOR BY C. ELEGAN	GLUTAMINE-DEPENDENT CA	GROWTH	GROWTH	GROWTH	GROWTH	CO8F1.1 PROTEIN.	COSMID ZC196.	F17A2.9.	F17A2.9.	HYPOTHETICAL PROTEIN (FIBROBLAST GROWTH FACT	B1549_F2_87.	CGRP-RECEPTOR COMPONEN	F46C3.3.	PROTEIN	133.0	DNA	SIALIDASE.		MMGC.	YRRI PROTEIN.	NISOYM	F15B9.1.

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RESULT ID RESULT AC P7 AC P7 AC P7 AC P7 DI O1 DI O1 DI O1 DI O1 DI O1 DE SI OC EK CO C EK CO 
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Best Local S
Matches
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Q63473; OF TREMBLREL. 01, CREATED;
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE (FRAGMENT).
                                                                                                                                                                                                                     MSRC-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAACOA; CHORDATA; VERTEBRATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P70366

PRELIMINARY; PRT; 1405 AA.

P70366;

01-FEB-1997 (TREMBLREL. 02, CREATED)

01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)

STEROID RECEPTOR COACTIVATOR-1.
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TISSUE-THYROID, AND PARATHYROID;
TISSUE-THYROID, GROSS G., MAYER H.;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.
NON_TER 1 1
SEQUENCE FROM N.A.
YAO T.P., KU G., ZHOU N., SCULLY R., LIVINGSTON D.M.;
PROC. NATL. ACAD. SCI. U.S.A. 93:10626-10631(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 AISEIQLM 29
::|||||
1 SVSEIQLM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 92.6%;
Local Similarity 75.0%;
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                                                                                                                                                                                                                                                                                                                    TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 105;
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DR EMDI; U64828; G1490876; ...
SO SEQUENCE 1405 AA; 152044 MW; 1743F755 CRC32;

QUETY MATCH
Best Local Similarity 83.3%, Score 45; DB 10; Length 1405;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 73 TVDGIQLH 80
OY 1 SVSEIQLH 8

Search completed: Thu Jul 30 10:01:39 1998

Job time: 40 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:05:09 1998; MasPar time 2.56 Seconds 41.911 Million cell updates/sec

Title: >US-08-817-547A-4
Description: (1-7) from US08817547A.pep
Perfect Score: 43
Sequence: 1 SVSEIQL 7

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.853; Variance 40.505; scale 0.342

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11111111111111111111111111111111111111	Result
2222222222222222222222222	Score
111111111111111111111111111111111111111	C C
200 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Length DB
W21948 W21947 P82176 W17949 W24273 W08131 W08131 R581367 R54367 R54367 R541551 P50517 P50517 P50517 P41554 P50517 P50517	Ħ
Fusion protein compri Fusion protein compri Sequence of parathyroid Human parathyroid hor Wild type parathyroid Human PTH derivative, Human PTH derivative, [Lys32]-hprH(1-34)-NH Human parathyroid hor Human parathyroid hor Fusion parathyroid hor Fusion parathyroid hor Fusion parathyroid hor Fusion parathyroid hor Sequence of methionin D-Ser3]hPTH (1-34)NH [Thr16]hPTH (1-34). Cyclised human parath Human pTH analogue [C Human parathyroid hor	Description
9.43e+01	Pred. No.

43 100.0 35 14 R74503 Parathyroid hormone p 43 100.0 35 14 R74509 Parathyroid hormone p 43 100.0 35 14 R74509 Parathyroid hormone p 43 100.0 35 14 R74509 Parathyroid hormone p 43 100.0 35 14 R74426 Parathyroid hormone p 43 100.0 36 9 R58212 {Ala17]-hpTH(1-36)-NP 43 100.0 36 9 R58212 {Ala17]-hpTH(1-36)-NP 43 100.0 36 9 R58277 {Nle189}-hpTH(1-36)-NP 43 100.0 36 9 R58277 {Nle189}-hpTH(1-36)-NP 43 100.0 36 9 R58257 {D-be34, D-Ala36]-hp 43 100.0 36 9 R58257 {D-be34, D-Ala36]-hp 43 100.0 36 9 R58227 {D-be34, D-PTH(1-36)-NP 43 100.0 36 9 R58213 {D-Ser17]-hpTH(1-36)-NP 43 100.0 36 9 R58213 {D-Ser17]-hpTH(1-36)-NP 43 100.0 36 9 R58213 {D-Ser17]-hpTH(1-36)-NP 43 100.0 36 9 R58134 {Ila19]-hpTH(1-38)-OP 43 100.0 38 9 R58134 {Ila19]-hpTH(1-38)-OP 43 100.0 38 9 R58141 {Leu21]-hpTH(1-38)-OP 43 100.0 38 9 R58159 {Nala27]-hpTH(1-38)-OP 43 100.0 42 26 P30015 Human parathyroid hor 43 100.0 44 26 P30015 Human parathyroid hor 43 100.0 84 27 W25687 Human parathyroid hor 43 100.0 84 27 W25687 Human parathyroid hor 43 100.0 84 28 R29565 Oxidation resistant p 43 100.0 84 5 R29563 Oxidation resistant p
0.0 35 14 R74503 Parathyroid ho 0.35 14 R74510 Parathyroid ho 0.35 14 R74509 Parathyroid ho 0.35 14 R74426 Parathyroid ho 0.35 14 R74426 Parathyroid ho 0.35 14 R74426 Parathyroid ho 0.35 14 R74425 Parathyroid ho 0.36 9 R58212 [Ala17]-hPTH(1 0.36 9 R58278 [D-Metl8]-hPTH(1 0.36 9 R58277 [Nle18]-hPTH(1 0.36 9 R58277 [D-Phe34, D-A1 0.36 9 R58277 [D-Ser17]-hPTH(1 0.36 9 R58213 [D-Ser17]-hPTH(1 0.36 9 R58214 [Ala19]-hPTH(1 0.36 9 R58214 [Ala19]-hPTH(1 0.36 9 R58214 [Leu21]-hPTH(1 0.36 9 R58314 [Leu21]-hPTH(1 0.38 9 R58114 [Leu21]-hPTH(1 0.38 9 R58134 [Val14]-hPTH(1 0.38 9 R58105 [Ala27]-hPTH(1 0
5 14 R74503 Parathyroid ho 5 14 R74510 Parathyroid ho 5 14 R74510 Parathyroid ho 5 14 R74426 Parathyroid ho 5 14 R74426 Parathyroid ho 5 14 R74426 Parathyroid ho 6 9 R58212 {Ala17}-hPH(1 6 9 R58277 {D-Met.18}-hPTH(1 6 9 R58277 {D-Phe34, D-A1 6 9 R58277 {D-Phe34, D-A1 6 9 R58227 {D-Sex17}-hPTH(1 6 9 R58214 {D-Sex17}-hPTH(1 8 9 R58134 {ILeu21}-hPTH(1 8 9 R5814 {ILeu21}-hPH(1 8 9 R5814 {ILeu21}-hPH(1 8 9 R58105 {Ala27}-hPTH(1 8 9 R58105 {Ala21}-hPTH(1 8 9 R58
4 R74503 Parathyroid ho 4 R74510 Parathyroid ho 4 R74510 Parathyroid ho 4 R74426 Parathyroid ho 4 R74426 Parathyroid ho 9 R58212 [Ala17]-hprH(1] 9 R58027 [Nuel8]-hprH(1] 9 R58277 [Nuel8]-hprH(1] 9 R58196 [D-pha34, D-A1] 9 R58196 [D-pha34, D-A1] 9 R58197 [D-pha34, D-A1] 9 R58197 [D-pha34, D-A1] 9 R58197 [D-pha]-hprH(1] 9 R58114 [Ja19]-hprH(1] 9 R58114 [Ja19]-hprH(1] 9 R58114 [Ja19]-hprH(1] 9 R58115 [Jala1]-hprH(1] 9 R58116 [Jala1]-hprH(1] 9 R58117 [Jala1]-hprH(1] 9 R58118 [Jala1]-hprH(1] 9 R58119 [Jala1]-hprH(1]-hprH(1] 9 R58119 [Jala1]-hprH(1]-hprH(1] 9 R58119 [Jala1]-hprH(1]-hprH(1]-hprH(1] 9 R58119 [Jala1]-hprH(
503 Parathyroid ho 503 Parathyroid ho 509 Parathyroid ho 426 Parathyroid ho 425 Parathyroid ho 426 Parathyroid ho 427 [Ala17]-hPTH(1 646 [L8,A16,D17,L1 646 [L-Phe34, D-A1 657 [M-Phe34, D-A1 657 [M-Sex17]-hPTH(1 657 [M-Sex17]-hPTH(1 658 [Ala19]-hPTH(1 659 [M-Sex17]-hPTH(1 659 [M-Sex
id ho id ho id ho id ho id ho id ho prid ho prid ll r r r r r r r r r r r r r r r r r r

88888888	388888	CC PT PT DR	PR PR PR PA	8 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT AC W AC W DT 3 DE F KW L
containing kanamycin and amplicilin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidine hydrochloride, and renatured by dilution in pH 7 phosphate buffer. The solution was clarified and the supernatant concentrated and purified on a column of immobilised intnoblotin. The purified material was incubated with tobacco etch virus (TEV) NIa protease and the PTH 1-37 fragment released, recovered by SA fragment	The parachyroid normone 1-3/ (PFH 1-3/) peptide with codon usage optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CORE, which contains the Met(13-139) streptavidin (SA) sequence, to give pSA-TEV-PTH. pSA-TEV-PTH and the LacIq repressor plasmid pUBS500 were used to transform E. coli KI2 RM82.	WPI; 97-289290/26. N-PSDB; T73912. N-PSDB; T89290/26. N-PSDB; T73912. N-PSDB; T7	14-A1. 1997. 1996; E04 1995; DE- BOEHRING	Synthetic. Synthetic. Homo sapiens. Location/Qualifiers Rey Peptide /note= "Met(13-139) streptavidin residue" Peptide /note= "linker cleavable by TEV NIB protease" Peptide 1016	1 21948; 21948; 0-JAN- 0-JAN- usion inker; usion

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Search completed: Thu Jul 30 10:05:25 1998 Job time : 16 secs.
                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant production of peptide(s) as fusions with streptavidin PT attached via cleavable linker - especially for urotropin and PT parathyroid hormone production

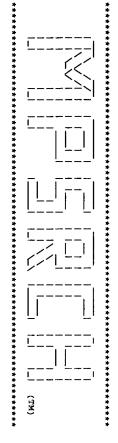
SE Example 3; Fig 3; 37pp; German.

CC The DNA encoding the present sequence, a linker and residues 1-7 of the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage for E. coli, was ligated to the 2.9 kb MheI-Hindiii CC (SA) sequence, to give psA-THRO-PTH. psA-THRO-PTH and the Lacig The transformants were grown, with IPTG induction, in medium and isolated inclusion bodies solubilised in guanidine containing kanamycin and ampilcilin. Cells were harvested, lysed hydrochloride, and renatured by dilution in pH 7 phosphate buffer. CC material was incubated with thrombin and the PTH 1-37 fragment CC material was incubated with thrombin and the PTH 1-37 fragment CC column followed by chromatography on a fractogel and reverse phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
ID W2
AC W2
DT 3(
DE FI
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Best Local
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                  14 svseigl 20
||||||||
1 SVSEIQL 7
                                                                                                                                                                                                          Sequence
                                                                                                                                   Y MATCH 100.0%;
Local Similarity 100.0%;
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T73911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kopetzki E;
WPI; 97-289290/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-1995; E04850.
16-NOV-1995; DE-042702.
(BOEF) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9718314-A1.
22-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W21947 standard; Protein; 20 AA.
W21947;
30-JAN-1998 (first entry)
Eusion protein comprising linker and PTH 1-37 (residues 1-7).
Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; thrombin.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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|||||||
1 SVSEIQL 7
                                                                                                                                                                                                      20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "linker cleavable by thrombin" /note= "parathyroid home......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Met(13-139) streptavidin residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "parathyroid homone 1-37 (residues 1-7)"
                                                                                                                       Score 43; DB 25; Length 20;
Pred. No. 9.43e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 25; Length 16;
Pred. No. 9.43e+01;
0; Mismatches 0; Indels
                                                                                                                       0,
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:04:35 1998; MasPar time 3.05 Seconds 83.806 Million cell updates/sec

bular output not generated.

Title: Description: Perfect Score: >US-08-817-547A-4 (1-7) from US08817547A.pep

Sequence: 1 SYSEIQL 7

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 19.518; Variance 19.793; scale 0.986

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22222222222222222222222222222222222222	Sult
3444444 344444 34444 3444 3444 3444 34	Score
100.0 100.0 100.	Query
34 37 37 31 31 31 115 115 896 896 896 105 105 119 998 3124 437 436 437 437	Length
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 	BB
1HTH 11WA 11HPH PTPG PTHU A05091 A05091 S76064 S76064 12WB 151851 C69611 A34694 A34937 S47179 A40020 S66952 S47179 A40170 S47179 A40170 S47179 A40170 S47179 A40170 S47179 A40170 S47179	Ħ
cyclic parathyroid ho parathyroid hormone (parathyroid hormone parathyroid hormone parathyroid hormone parathyroid hormone parathyroid hormone parathyroid hormone phycobilisome anchor parathyroid hormone (parathyroid hormone (parathyroid hormone (parathyroid hormone (parathyroid hormone parathyroid hormone phycothetical protein cull protein protein collagen alpha 1(XII) hypothetical protein collagen ase protein collagenase protein nitrogenase (EC 1.18.	Description
2.97e+00 2.97e+00 2.97e+00 2.97e+00 2.97e+00 9.26e+00 9.26e+00 9.26e+01 2.77e+01 4.72e+01 4.72e+01 4.72e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
3 6	3 6	3 6	36	3 6	36	ω 6	36	36	36	36	<u>ა</u>	<u>з</u>	37	37	37	37	37	37	37	37	37
83.7	83.7	w	w	w	ω	83.7	w	83.7	w	83.7	w	w	g	S)	CD)	CD.	O	α	O	86.0	a
1150	1070	989	553	399	381	372	367	366	350	335	116	115	1132	1116	764	615	605	492	478	478	438
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S49956	A54600	I56333	G1BPSV	E33282	S65212	D64716	I39649	139518	B39364	S35126	S22553	JC4202	JC4127	S41915	A49448	A05269	S36592	NIAVMA	1N2CA	1N2CC	A55070
probable membrane pro	phosphatidylinositol	₽	gene 1 protein - spir	prot	hypothetical protein	regulatory protein Dn	lipoprotein - Actinob	lipoprotein - Actinob	GDF-1 embryonic growt	anthranilate phosphor	Ig heavy chain V regi	parathyroid hormone -	protein-tyrosine kina		3	collagen alpha 1(III)	El protein - human pa	nitrogenase (EC 1.18.	nitrogenase molybdenu	nitrogenase molybdenu	DNA primase (EC 2.7.7
1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01

Resolu Determ		structure of human structures structures #formal_name Homo A67856	RESULT 2 ENTRY IITLE parathyroid hormone (residues 1-34) - human ALTERNATE NAMES HPTH(1-34)	Db 1 SVSEIQL 7	Query Match 100.0%; Score 43; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 2.97e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#region helix (right hand 3-10)\ 4-6 #region helix (right hand alpha) 20-29 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4146 #checksum 5768	#CTOSS-TETETENCES PUB:LHTH COMMENT Resolution: not applicable COMMENT Determination: NMR COMMENT cyclic; human parathyroid hormone; norleucine NMR structure; VERNORDS cyclic; human parathyroid hormone; norleucine NMR structure; Ornithine	#authors Roesch, P.; Seidel, G.; Schaefer, W.; Esswein, A.; Hofmann, E. #submission submitted to the Brookhaven Protein Data Bank, April 1997	PDB_TITLE the solution structure of cyclic human parathyroid hormone fragment 1 - 34, NMR, 10 structures ORGANISM #formal_name synthetic REFERENCE A68105	
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	Search completed: Thu Jul 30 Job time : 16 secs.	Db 1 SVSEIQL Oy 1 SVSEIQL	Query 1 Best Lo Matches	6-9 19-30 SUMMARY	KEYWORDS FEATURE
	Thu Jul 30 10:04:51 s.	7		#region heli: #region heli: #length 34 #mole:	hormone
	:51 1998		Score 43; DB 5; Length 34; Pred. No. 2.97e+00; 0; Mismatches 0; Indels	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum !</pre>	
			0;	5629	
			Gaps		
			0;		

(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

in on: bular output not generated. Thu Jul 30 10:03:18 1998; MasPar time 2.05 Seconds 85.496 Million cell updates/sec

Sequence: Description: Perfect Score: Title: >US-08-817-547A-4 (1-7) from US08817547A.pep 43 1 SVSEIQL 7

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics:

Mean 20.233; Variance 16.121; scale 1.255

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	BB	Ħ	Description	Pred. No.
1	43	100.0	115	ָׁ ב	PTHY_HUMAN	PARATHYROID HORMONE PR	3.67e-01
2	43	100.0	115	1		HORMONE	3.67e-01
ω	41	95.3	115	_	PTHY_RAT	PARATHYROID HORMONE PR	1.46e+00
4	41	95.3	896	Ļ	APCE_SYNY4	PHYCOBILISOME 100.5 KD	
տ	39	90.7	567	_	CYDC_BACSU	TRANSPORT ATP-BINDING	5.55e+00
o	39	90.7	1827	_	CUT1_SCHPO	CUT1 PROTEIN.	5.55e+00
7	38	88.4	119	_	PTHY_CHICK	PARATHYROID HORMONE PR	1.06e+01
&	38	88.4	3124	μ	CA1C_CHICK	COLLAGEN ALPHA 1(XII)	1.06e+01
9	37	86.0	407	۲	Y090_METJA	PUTATIVE PROTEASE MJ00	1.98e+01
10	37	O	438	_	PRI1_DROME	DNA PRIMASE 50 KD SUBU	1.98e+01
11	37	86.0	491	۲	NIFD_AZOVI	NITROGENASE MOLYBDENUM	1.98e+01
12	37	ത	605	μ	VE1_HPV09	REPLICATION PROTEIN E1	1.98e+01
13	37	86.0	615	Н	CA13_CHICK	COLLAGEN ALPHA 1(III)	1.98e+01
14	37	86.0	675	Н	VPS5_YEAST	VACUOLAR PROTEIN SORTI	1.98e+01
15	37	σ	764	_	ICCR_DROME	IRREGULAR CHIASM C-ROU	1.98e+01
16	37	σ	1116	μ	RPOB_HETCA	DNA-DIRECTED RNA POLYM	1.98e+01
17	37	σ	1132	Н	JAK2_RAT	TYROSINE-PROTEIN KINAS	1.98e+01
18	37	86.0	1145	۳	DPOG_DROME	DNA POLYMERASE GAMMA (1.98e+01
19	36	83.7	115	۳	PTHY_CANFA	PARATHYROID HORMONE PR	3.66e+01
20	36	ω	282	μ	DAAA_STAHA	D-ALANINE AMINOTRANSFE	3.66e+01
21	36	83.7	335	<u>بر</u>	TRPD_LACLA	ANTHRANILATE PHOSPHORI	3.66e+01
22	36	ω	350	ب	UOG1_MOUSE	HYPOTHETICAL UOG-1 PRO	3.66e+01
23	36	83.7	392	-	HRC2_CHLTR	HEAT-INDUCIBLE TRANSCR	3.66e+01

44 45	42 43	41	40	39	38	37	36	35	34	<u>ω</u> ω	32	31	30	29	28	27	26	25	24
35 5	3 3 5 5	35	ω 5	ß	3 5	ω 5	<u>3</u>	35	35	35	36	36	ω 6	36	36	36	3 6	36	36
81.4 81.4	81.4 81.4	•	81.4	٠	81.4	٠	81.4	81.4	•	81.4	83.7	٠	•	83.7		83.7			
1167 2109	1036	853	760	679	500	464	325	314	303	262	1150	1070	1047	859	857	832	553	537	393
_		_	μ		بر	<u>س</u>	Н	_	سا	<u>س</u> و	<u>, , , , , , , , , , , , , , , , , , , </u>	۳	<u>_</u>	ب	ب	Ь	ш	ب	\vdash
ITAE_MOUSE RRPL_VSVSJ	P200_MYCPN	PXA2_YEAST	YCE5_YEAST	PBP2_STRPN	ZIPP_DROME	WCAM_ECOLI	SYK3_ECOLI	REPE_STAAU	Y367_HAEIN	FLGG_CAUCR	YIC6_YEAST	P11B_HUMAN	YBDE_ECOLI	YQD3_CAEEL	CLPB_ECOLI	KLP1_SCHPO	VG1_SPV4	ZO29_XENLA	THIL_RHIME
INTEGRIN ALPHA-E PRECU RNA POLYMERASE BETA SU	PROBABLE SENSOR PROTEI PROTEIN P200.	LONG	HYPOTHETICAL 87.2 KD P	PENICILLIN-BINDING PRO	ZIPPER PROTEIN PRECURS	COLANIC ACID BIOSYNTHE	HYPOTHETICAL LYSYL-TRN	REPLICATION INITIATION	HYPOTHETICAL PROTEIN H	FLAGELLAR BASAL-BODY R	HYPOTHETICAL 133.0 KD	PHOSPHATIDYLINOSITOL 3	HYPOTHETICAL 114.7 KD	HYPOTHETICAL 96.7 KD P	CLPB PROTEIN (HEAT SHO	KINESIN-LIKE PROTEIN 1	CAPSID PROTEIN.	OOCYTE ZINC FINGER PRO	ACETYL-COA ACETYLTRANS
6.65e+01 6.65e+01	6.65e+01 6.65e+01	•	•	6.65e+01	6.65e+01	•	6.65e+01	6.65e+01	6.65e+01	•	3.66e+01	•	•	3.66e+01	3.66e+01	•	3.66e+01	3.66e+01	3.66e+01

RRERE	RRR	R R A	R R	7 7 7 7 7 7	R R	RA X	RP	P. P.	R.	RX X	RN	RL	RA	RX	RP	RN	2 2	₹ ₹	RP	R C	38	SO	GN	DE .	3 5	3 5	ΑC	RESULT
(IN) CALCIUM REGULATING HORMONES, TALMADGE R.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975). [7]	ALL H.D.,	POTTS J.T. JK.; BIOCHEMISTRY 17:5723-5729(1978). [6]			O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.; PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).	SAUER R.T., JACOBS J.W., KEUTM	SEQUENCE OF 32-68.	249:155-157(1974).	. W	SEQUENCE OF 26-37.		NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983)	VASICEX T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J., HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;	1834.			DROC NAME. ACCIDED A.M., FOLLS SIL. SR., MICH SI.	NE; 82150870.	UENCE	[1]	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	SAPIENS (HUMAN)		HORMONE PR	11-AOG-1907 (REL. CO, LAGI DECCEDENCE CEDATE)	01, CREATED)		LT 1 PTHY HUMAN STANDARD: PRT: 115 AA.

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SO SECTION OF SECTION 
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Best Local S
Matches
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91009911.
ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A., KRONENBERG H.M.;
J. CLIN. INVEST. 86:1084-1087(1990).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS BONE AND PREVENTING THEIR RENAL EXCRETION.
-1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED HYPOPARATHYROLDISM (FIH).
EMBL; J00301; G190704; -.
EMBL; J00301; G190704; -.
EMBL; A29146; E186700; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95318084.
MARX U.C., AUSTERMA
STICHT H., WALTER S
ROESCH P.;
                                                                                                                                                                                                                                                                                                                 HORMONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A01536; PTHU.
PIR; A19339; A19339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRÜCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 32-68 MEDLINE; 95318084.
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ANDREATTA R.H., HARTMANN A., JOEHL A.,
ANDREATTA R.H., HARTMANN A., JOEHL A.,
RINIKER B., RITTEL W., SIEBER P.;
HELV. CHIM. ACTA 56:470-473(1973).
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TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D., KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J. HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE: 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
BIOCHEMISTRY 14:1842-1847(1975).
[8]
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1HTH;
1ZWA;
1ZWB;
1ZWC;
1ZWC;
1ZWE;
1ZWE;
1ZWF;
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SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
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12-MAR-97.
16-JUN-97.
16-JUN-97.
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15-OCT-97.
12-MAR-97.
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115
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12-MAR-97.
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SCHMID F.-X.,
                                                                                                                                  W.
         Score
Pred.
0; M
                                                                                                                   PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEF)
PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
; 243E87C7 CRC32;
            Mismatches
                                  43; DB 1; 1
No. 3.67e-01
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JAENICKE
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         Indels
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FORSSMANN W.-G.,
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      Gaps
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RESULTATION AND PROPERTY OF SOLUTION AND PROPE
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A SAUER R.T., NIALL H.L.,
A POTTS J.T. JR.;
L BICCHEMISTRY 13:1994-1999(1974).
L BICCHEMISTRY 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVARIES CALCIUM LEVEL BY DISSOLVING THE BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; XO5722; G1839; -.
DR PIR; A01535; PTPG.
DR PIR; B26806. B26806.
PPR PROSITE; PS00335; PARATHYROID; 1.
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Search completed: Thu Job time: 7 secs.
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PROPEP
CHAIN
SEQUENCE
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PO1269;
PO1269;
PO1269;
21-JUL-1986
O1-JAN-1988
O1-FEB-1996
PARATHYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 26-115.

MEDLINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 87316938. SCHMELZER H.-J., G
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EUKARYOTA; METAZOA; CHO
EUTHERIA; ARTIODACTYLA.
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MEDLINE; 74253317.
                                                                                                                                       32
                                                                                       1 SVSEIQL
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1 SVSEIQL
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larity 100.0%;
Conservative
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12852 MW;
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06, LAST SEQUENCE UI
33, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSS G., WIDERA G.,
15:6740-6740(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6, LAST SEQUENCE UPDATE)
3, LAST ANNOTATION UPDATE)
PRECURSOR (PARATHYRIN) (P
                     30
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                     10:03:25
                                                                                                                                                                         Score 43; DB 1;
Pred. No. 3.67e-01
0; Mismatches
                                                                                                                                                                                                                                                                     PARATHYROID HORMONE 98B67F47 CRC32;
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                     1998
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Statistics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bular output not generated.
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                                                                                                                                                                                                                                                                                 ĕ
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
  protein - protein database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                                Match
 PAM 150
Gap 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                >US-08-817-547A-4
(1-7) from US08817547A.pep
43
                                                                                                                                                                                                                                                                                                                                                                                                                           sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                     Mean 19.611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140542 segs, 42109429 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thu Jul 30 10:03:43 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVSEIQL 7
                                                                                                                                                                                                                                                                               Length
 930
1145
1810
2089
3456
101
189
356
                                                                                                                                 459
717
958
987
691
714
  В
                                                                                                                                                                                                                                                                                                                                                                                                     Variance 15.404; scale 1.273
016546
0013724
041942
040554
090794
090794
0935804
P70593
0243103
0294906
018038
0194676
019478
019478
0414616
                                                                                                                                                                                                                           Q55544
Q63473
P93756
                                                                                                                                                                                                                                                                               Ħ
                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MasPar time 3.80 Seconds 77.626 Million cell updates/sec
                                                                           DNA POLYMERASE GAMMA (CODED FOR BY C. ELEGAN KIAA0170 PROTEIN.
                                                                                                                   ALPHA-1 TYPE III COLLA JANUS PROTEIN TYROSINE A-KINASE ANCHORING PROMGPS.
                                                                                                                                                                                                               HYPOTHETICAL 100.3 KD PARATHYROID HORMONE (F RECEPTOR-LIKE PROTEIN C35All.2 PROTEIN.
 LIPOPROTEIN PRECURSOR.
            HYPOTHETICAL 23.4 KD YBGE PROTEIN.
                                      (FRAGMENT).
F15B9.1.
                                                                                                                                                                                      HYPOTHETICAL 51.4 KD PHYPOTHETICAL 82.9 KD P
                                                                                                                                                                                                                                                                               Description
                                                                 POLYPROTEIN.
1. 43e+00

5. 71e+00

5. 71e+00

1.12e+01

1.12e+01

1.12e+01

1.12e+01

1.12e+01

1.12e+01

2.16e+01

4.10e+01

4.10e+01

4.10e+01

4.10e+01

4.10e+01
                                                                                                                                                                                                                                                                               Pred.
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RESU DT DT D	Que Bes Mat Db	SORPRARE		RESUL	
Q63473 Q6	ry Ma t Loc ches 562	SEQUENCE FE SEQUENCE FE STRAIN-PCC6 MEDLINE; 96 KANEKO T., SUGIURA M., SUGIURA M., DNA RES. 2: EMBL; D6399 HYPOTHETICA SEQUENCE	O1-NOV-1996 (T O1-NOV-1996 (T O1-NOV-1996 (T HYPOTHETICAL 1 SLR0335. SYNECHOCYSTIS PROKARYOTA; BA CYANOBACTERIA;	7LT Q5554	44444433333333333222222222222222222222
2 3 3 7 7 199 199 199 199 199 199 199 199 199	ch 1 s 1 s VAE	NCE FROM N=PCC68 N=PCC68 NE; 961 O T., 7 RA M., 7 ES. 2:1 ES. 2:1 L63999 HETICAL	V-1991 V-1991 V-1991 HETIC: 35: HOCYS: RYOTA BACTE!		
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א מממ מ	95.3 ty 85.7 servativ	29. SAT. KA A., SAT. ATA S.; 166(1995). 1001419; COTEIN. AA; 10029	MBLREL. MBLREL. MBLREL3 KD P . ERIA; G	PRELIMINARY	3457 3467 3467 10889 110889 1150 21557 15157 4479 4479 4479 4479 4479 4479 4479 44
MINARY; EL. 01, C EL. 05, L EL. 05, L CFRAGMENT AT). CHORDATA;	** **	и . O	GRACILI	AL RY;	00100011110000000000000000000000000000
PRT REAT AST AST VER	Score 41; Pred. No. 1; Misma	., KOTANI W; EE614	REAJ AST AST	LIGNMENTS PRT;	0244164 026092 026092 026093 0263052 0263052 02630552 02630552 0265115
; 105 AA. ED) SEQUENCE UPDATE) ANNOTATION UPDATE) TEBRATA; TETRAPODA; MAMMALIA;	; DB 9; Length 896; b. 1.43e+00; matches 0; Indels 0;	II H., SAZUKA T., MIYAJIMA N	ED) SEQUENCE UPDATE) ANNOTATION UPDATE) S; OXYPHOTOBACTERIA;	'S 896 AA.	REGULATORY PRECURSOR. REGULATORY PROTEIN DNI CHROMOSOME XVI READING HYPOTHETICAL 42.6 KD PAPOLIPOPROTEIN B (FRAG HYPOTHETICAL 133.0 KD POLYPETIDE. PEPTIDE SYNTHETASE. PENICILLIN-BINDING PRO F56D6.3. B0564.3. B0564.3. PENICILLIN-BINDING PRO (STRAIN VAI) PENICILLI (STRAIN WAI) PENICILLI (STRAIN WAI) FOR COLUMN (STRAIN WAI) PENICILLI (STRAIN KAGUANE/73) PE PENICILLIN BINDING PRO PENICILLIN
	Gaps 0;				4.10e+01 4.10e+01 4.10e+01 4.10e+01 4.10e+01 4.10e+01 4.10e+01 4.10e+01 7.66e+01

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RC TISSUE-THYROID, AND PARATHYROID;
RA SCHMELZER H.J., GROSS G., MAYER H.;
RL ADV. GERE TECHNOL. 21:229(1994).

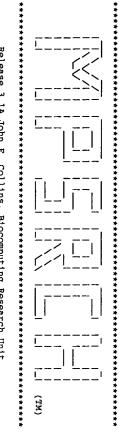
DR EMBL, M54875; G601933; -
FT NON_TER
SO SEQUENCE 105 AA; 11746 MM; 6AC3163E CRC32;

QUETY MATCH
Best Local Similarity 71.4%; Pred. No. 5,71e+00;
MATCHES 5; CONSERVATIVE 2; Mismatches 0; Indels 0; Gaps 0;

DD 22 AISEIOL 28
::|||| 1|
QY 1 SYSEIOL 7

Search completed: Thu Jul 30 10:04:16 1998

JOB time: 33 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:07:26 1998; MasPar time 2.53 Seconds 36.409 Million cell updates/sec

fbular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-5 (1-6) from US08817547A.pep 35 1 SVSEIQ 6

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.234; Variance 31.551; scale 0.388

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match Le	Length	B	ID	Description	Pred. No.
1	35	100.0	16	25	W21948	Fusion protein compri	2.24e+02
2	35	100.0	20	25	W21947	_	2.24e+02
ω	35	100.0	ω ω	ω	P82176	н	2.24e+02
4	35	100.0	34	4	R22293	Human parathyroid hor	2.24e+02
5	35	100.0	34	22	W19994		2.24e+02
თ	35	100.0		22	W17962	Human PTH analogue [C	2.24e+02
7	35	100.0		22	W17961	Human PTH analogue [C	2.24e+02
œ	35	100.0	34	22	W17960	Human PTH analogue [C	2.24e+02
9	35	100.0		œ	R41561	[Lys16, Gln27]hPTH (1	2.24e+02
10	35	100.0	34	9	R58054	[L8,A17,Q18,A19,R22,T	2.24e+02
11	35	100.0	34	9	R58193	[L8,D10,K11,T33,A34]-	2.24e+02
12	35	100.0	34	w	P50517	Sequence of methionin	2.24e+02
13	35	100.0	34	œ	R41549	[D-Ser3]hPTH (1-34)NH	2.24e+02
14	35	100.0	34	æ	R41551	[Thr16]hPTH (1-34).	2.24e+02
15	35	100.0	-	φ	R58232	[Lys32]-hPTH(1-34)-NH	2.24e+02
16	35	100.0	-	22	W17966	Human PTH analogue [C	2.24e+02
17	35	100.0	-	22	W17939	Human parathyroid hor	2.24e+02
18	35	100.0	-	22	W17951	Human parathyroid hor	2.24e+02
19	35	100.0	35	14	R74504		2.24e+02

4.4	<u> </u>	43	42	41	40	39	38	37	36	35	34	သ	32	31	30	29	28	27	26	25	24	23	22	21	20
35	ب ا ار	ա	35	35	35	3 5	35	35	<u>ω</u>	ა 5	35	3 5	35	35	35	35	ω	35	ω 5	35	35	35	35	35	35
100.0			•		•	•			•	•		•	•		•	•		•	•	•	•	•	•	•	•
102																									
40	ю.	4	ഗ	25	G	G	27	25	26	10	ø	ø	ø	9	ဖ	9	9	9	φ	ω	ø	14	14	14	14
P40252	BA3073		884	W29420	R29565	R29563	W25687	W21946	\mathbf{r}	R54234	R58116	R58115	R58157	R58141	R58103	R58214	R58213	823	R58055	R58046	R58200	R74417	R74418	R74510	R74503
Protein including hum		Bovine parathyroid ho	Oxidation resistant [Human parathyroid hor	Oxidation resistant [Oxidation resistant P	Human parathyroid hor	Fusion protien compri	Human parathyroid hor	PTH N-terminal.	16]-hPTH(1-	6]-hPTH(1-	27]-hPTH(1-38)-	1]-hPTH(1-38)-	hPTH(1-38)-	9]-hPTH(1-36)-	[D-Ser17]-hPTH(1-36)-	ŝ	Q18]-hPTH(1-36)	[L8,A16,D17,L18,A19]-	[D-H1s9]-hPTH(1-36)-N	hormone	hormone	Parathyroid hormone p	Parathyroid hormone p
2.24e+02	3 346+03			2.24e+02		•	•	2.24e+02		•	٠	٠			•	'n	١,	:،	'n	•	:.	:.	٠	2.24e+02	٠,

88	88	88	გ	ရှိ	38	38	8	S	8	2 5	לי ני ניו ני	ΡŢ	DR	DR	ΡĮ	PΑ	PR	PF	8	Š	H	Ţ	H	FT	Ŧ	F	Į Į	ည	လ္လ	Š	Ž.	Z E	Ţ	AC	ij	RESULT
		and isolated inclusion bodies solubilised in guanidine hydrochloride, and renatured by dilution in pH 7 phosphate buffer.	containing kanamycin and ampilcilin. Cells were harvested, lysed		repressor plasmid pUBS500 were used to transform E. coli K12 RM82.	ment of pSAM-C	optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII	the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage	The DNA encoding the present sequence, a linker and residues 1-7 of	Francis 4: Fig 3: 37on German	attached via cleavable linker - especially for urotropin and	F.		WPĪ; 97-289290/26.	E.	7		06-NOV-1996; E04850.	22-MAY-1997.	•		1				tide		Homo sapiens.	Synthetic		rotein: recombinant	<pre>!!nker: parathyroid hormone 1-37: PTH 1-37: streptavidin:</pre>	1998 (first entry)	••	W21948 standard; Protein; 16 AA.	JLT 1

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Search completed: Thu Jul 30 10:07:41 1998 Job time: 15 secs.
                                                                                                                                                                                                                                                                                                                                                                                               8888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
ID W2
AC W2
DT 3C
DE FL
                                                                                                                                                                                                         PT Recombinant production of peptide(s) as fusions with streptavidin PT attached via cleavable linker - especially for urotropin and PT parathyroid hormone production
PS Example 3; Fig 3; 37pp; German.
CC The DNA encoding the present sequence, a linker and residues 1-7 of CC the parathyroid hormone 1-37 (PFH 1-37) peptide with codon usage CC contains to for E. coli, was ligated to the 2-9 kb Nhel-HindlII CC (SA) sequence, to give pSA THRO-PTH. DSA-THRO-PTH and the LacIg repressor plasmid pUBS500 were used to transform E. coli kl2 RM82. Containing kanamycin and ampilcilin. Cells were harvested, lysed containing kanamycin and ampilcilin. Cells were harvested, lysed containing kanamycin and ampilcilin. Cells were harvested, lysed containing kanamycin and ampilcilin glandiane CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer. The solution was clarified and the supernatant concentrated and cc material was incubated with thrombin and the PTH 1-37 fragment cc column followed by SA fragment removal on an iminobiotin cc cupum followed by chromatography on a fractogel and reverse phase solubles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
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                                                                                                                                       Matches
                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duery Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09718314-A1.
22-MAY-1997.
06-NOV-1996; E04850.
16-NOV-1995; DE-042702.
(BOEF) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kopetzki E;
WPI; 97-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rusion protein comprising linker and PTH 1-37 (residues 1-7). Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; thrombin. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UT 2
W21947 standard; Protein; 20 AA.
W21947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                       14 svseig 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T73911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              removal on an iminobiotin column fractogel and reverse phase HPLC. Sequence 16 AA;
                                                                                                                                  Y Match 100.0%;
Local Similarity 100.0%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                   1 SVSEIQ 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVSEIQ 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97-289290/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Met(13-139) streptavidin residue" 2.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "linker cleavable by thrombin" 14..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "parathyroid homone 1-37 (residues 1-7)"
                                                                                                                            Score 35; DB 25; Le
Pred. No. 2.24e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 25; Length 16; Pred. No. 2.24e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       followed by chromatography on
                                                                                                                                                             Length 20;
                                                                                                                              Indels
                                                                                                                            0,
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                                                                                                                           Gaps
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:06:50 1998; MasPar time 3.00 Seconds 73.160 Million cell updates/sec

bular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-5 (1-6) from US08817547A.pep 35 1 SVSEIQ 6

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 17.547; Variance 15.799; scale 1.111

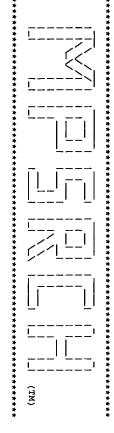
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sult No.	Score	Query Match	Length 1	BB	ID	iptio	ı > :
1	35	100.0	34	տ	1HTH	cyclic parathyroid ho	2.66e+01
N	35	100.0	34	v	1ZWA	~	o
ω	35	100.0	37	σ	1HPH		•
4	35	100.0	115	N	JC4202	parathyroid hormone -	2.66e+01
ر.	35	100.0	115	μ.	PTHU	parathyroid hormone p	
6	35	100.0	115	<u>بــر</u>	PTPG	hormone	
7	35	100.0	303	2	A64150	1 protein	2.66e+01
æ	35	100.0	853	N	S34682	=	
9	35	100.0	1116	N	S41915	О	2.66e+01
10	33	94.3		u	12WC	parathyroid hormone (8.67e+01
11	33	94.3		Н	PTBO	parathyroid hormone p	8.67e+01
12	33	94.3		N	A05091	hormone	8.67e+01
13	33	94.3		N	E69400	3-hydroxyacyl-CoA deh	
14	33	94.3	424	N	139310	zinc finger protein Z	8.67e+01
15	33	94.3	428	ν	A42311	A-kinase anchor prote	8.67e+01
16	33	94.3	540	2	S35071	auxin-resistance prot	8.67e+01
17	33	94.3	801	N	PC6010	RNA helicase Gu - hum	8.67e+01
18	33	94.3	896	N	S59990	phycobilisome anchor	8.67e+01
19	33	94.3	896	N	S76064	hypothetical protein	8.67e+01
20	32	91.4	270	N	B32835	hypothetical ntrA pro	1.53e+02
21	32	91.4	329	N	G69210	pothet	1.53e+02
22	32	•	422	N	A34589	lin-10 protein - Caen	1.53e+02
23	32	91.4	507	N	в69957	conserved hypothetica	1.53e+02

45	44	43	42	41	40	39	38	37	36	35	34	ယ	32	31	30	29	28	27	26	25	24
31	31	31	31	31	31	31	31	3	31	ω H	31	31	31	31	31	31	3	31	3 1	32	32
8	œ	φ.	8	œ	8	8	8		8		8	8	œ	88.6		8	8		æ		91.4
3066	1039	994	677	635	416	415	402	392	298	259	259	259	259	259	259	259	146	109	109	697	537
μ	N	N	N	N	N	N	N	N	N	σ	ű	σ	ហ	u	ഗ	σ	N	ഗ	σ	N	2
JQ1662	S02711	A47474	S33664	S19011	C47017	S63221	S47329	A69474	S76437	1TOCH	IVITH	LUCYK	LUCYN	1BBRK	1TBQK	1TBQH	S76533	LUCYE	IVITG	G70133	S50344
genome polyprotein -	cellulase (EC 3.2.1.4	ADP-ribosyltran	flagella-associated p	endo-1,4-beta-xylanas	probable transcriptio	DNA-directed RNA poly	_		hypothetical protein	thrombin (EC 3.4.21.5	alpha thrombin (EC 3.	n (EC 3.4.21.	thrombin (EC 3.4.21.5	_	thrombin (EC 3.4.21.5	thrombin (EC 3.4.21.5	hypothetical protein	thrombin (EC 3.4.21.5	epsilon thrombin (EC	flagellar biosynthesi	aspergillopepsin homo
٠		2.66e+02		٠	2.66e+02	2.66e+02	٠	•	٠	٠	2.66e+02		2.66e+02	2.66e+02	2.66e+02		٠	•		1.53e+02	

	Search complete Job time : 18 s	Db 1 SVSEIQ Qy 1 SVSEIQ	Query Match Best Local Si Matches 6	FEATURE 6-9 19-30 SUMMARY	KEYWORDS
	Search completed: Thu Jul 30 10:07:08 1998 Job time : 18 secs.	σ σ	Query Match 100.0%; Score 35; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 2.66e+01; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#region helix (right hand alpha)\ #region helix (right hand alpha)\ #length 34 #molecular-weight 4118 #checksum 5629	hormon



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:05:44 1998; MasPar time 2.12 Seconds 70.907 Million cell upda updates/sec

bular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-5 (1-6) from US08817547A.pep 35 1 SVSEIQ 6

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match Listing first 4.5 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 18.271; Variance 12.955; scale 1.410

and is derived by a Pred. No. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES

esult	Score	Query Match	Length	BB	ID	Description	Pred. No.
-	35	100.0	115	ㅁ :	PTHY_PIG	PARATHYROID HORMONE PR	5.84e+00
N	35	•	115	\vdash	LŤΙ	HORMONE P	٠
w	35	100.0	115	μ.	PTHY_HUMAN	PARATHYROID HORMONE PR	5.84e+00
4	35	100.0	303	Н	Y367_HAEIN	HYPOTHETICAL PROTEIN H	5.84e+00
տ	35	٠	853	-	PXA2_YEAST	PEROXISOMAL LONG-CHAIN	5.84e+00
σ	35		1116	μ	RPOB_HETCA	DNA-DIRECTED RNA POLYM	•
7	33		112	دسو	GLNB_MYCTU	NITROGEN REGULATORY PR	2.41e+01
œ	33	94.3	115	μ.	PTHY_RAT	PARATHYROID HORMONE PR	2.41e+01
9	33	94.3	115	H	PTHY_BOVIN	PARATHYROID HORMONE PR	2.41e+01
10	33	94.3	370	<u>سر</u>	CPR3_CAEEL	CATHEPSIN B-LIKE CYSTE	2.41e+01
11	33	94.3	428	μ.	AK75_BOVIN	A-KINASE ANCHOR PROTEI	2.41e+01
12	33	94.3		ш	AXR1_ARATH	AUXIN-RESISTANCE PROTE	2.41e+01
13	33	94.3		<u>د ب</u>	APCE_SYNY4	PHYCOBILISOME 100.5 KD	2.41e+01
14	32	۲	270	۳	YHBG_RHIME	PROBABLE ABC TRANSPORT	4.75e+01
15	32		417	Н	LI10_CAEEL	LIN-10 PROTEIN.	4.75e+01
16	32	91.4	507	Н	YQGP_BACSU	HYPOTHETICAL 56.4 KD P	4.75e+01
17	32	۲	537	щ	YIV9_YEAST	PUTATIVE ASPARTYL PROT	4.75e+01
18	31	88.6	164	\vdash	Y646_METJA	HYPOTHETICAL PROTEIN M	9.18e+01
19	31	8	180	ш	RE15_SCHPO	MEIOTIC RECOMBINATION	9.18e+01
20	31	8	282	۳	VIT4_CAEEL	VITELLOGENIN 4 PRECURS	9.18e+01
21	31	8	402	μ	OXA1_YEAST	CYTOCHROME OXIDASE BIO	9.18e+01
22	31	8	415	بر	RPA3_YEAST	DNA-DIRECTED RNA POLYM	9.18e+01
23	31	8	416	-	RPSC_ANASP	RNA POLYMERASE SIGMA-C	9.18e+01

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1 SYSEIQ

σ

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	3 1	30	29	28	27	26	25	24
30	30	30	30	30	30	30	30	30	31	31	31	31	31	31	31	31	31	3	31	31	31
	85.7	85.7	85.7	85.7	85.7	85.7	85.7	s.	8	8	88.6	8	8	8		œ	œ	œ	°	88.6	œ •
2412	2329	1131	982	381	342	275	265	115	1827	1039	994	937	804	727	677	635	625	809	602	594	567
, بر	_	ب	Н	Ц	_	<u>, , </u>	_	<u> </u>	щ	_	ب	ᆫ	Н	μ	4سم	ш	μ	\vdash	ب	Н	ш
POL1_BAYMG	YS89 CAEEL	YMS2_CAEEL	YS96_CAEEL	PTX3_MOUSE	YM22_YEAST	POR1_WHEAT	FAEH_ECOLI	YSCI_YEREN	CUT1_SCHPO	GUNB_CALSA	PPOL_DROME	ODO1_BACSU	CADD_STAAU	CADA_STAAU	FLHA_BACSU	XYND_BACPO	THRB_BOVIN	RDPO_SCEOB	VE1_HPV15	RBJK_DROME	CYDC_BACSU
ROTEIN	HYPOTHETICAL 254.3 KD	PUTATIVE ATP-DEPENDENT	HYPOTHETICAL 110.4 KD	PENTAXIN-RELATED PROTE	HYPOTHETICAL 38.6 KD P	OUTER MITOCHONDRIAL ME	K88 MINOR FIMBRIAL SUB	YOP PROTEINS TRANSLOCA	CUT1 PROTEIN.	ENDOGLUCANASE B PRECUR	POLY (ADP-RIBOSE) POLY	2-OXOGLUTARATE DEHYDRO	PROBABLE CADMIUM-TRANS	PROBABLE CADMIUM-TRANS	FLAGELLAR BIOSYNTHESIS	ENDO-1,4-BETA-XYLANASE	PROTHROMBIN PRECURSOR	PROBABLE REVERSE TRANS	REPLICATION PROTEIN E1	J KAPPA-RECOMBINATION	TRANSPORT ATP-BINDING
1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01

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SOUR PRODUCT P
밁
                                                                                     Query Match
Best Local (
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTHY_PIG
P01269;
21-JUL-1986
01-JAN-1988
01-FEB-1996
                                                                                                                                                                               SIGNAL
PROPEP
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                              SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
POTTS J.T. JR.;
BIOCHEMISTRY 13:1994-1999(1974).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL; X05722; G1839; -.
EMBL; X05722; G1839; -.
EMBL; X05722; G1839; -.
PIR; A01535; PTPG.
PIR; B26806, B26806.
PROSITE: PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARATHYROID HORMO
PTH.
SUS SCROFA (PIG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 32-115. MEDLINE; 74253317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-115.
MEDLINE; 76018954.
CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W.,
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 87316938.
SCHWELZER H.-J., GROSS G., WIDERA G., MAYER
NUCLEIC ACIDS RES. 15:6740-6740(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                         Match 100.0%;
Local Similarity 100.0%;
nes 6; Conservative
32 SVSEIQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74253317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 (REL. 01, CREATED)
8 (REL. 06, LAST SEQU
6 (REL. 33, LAST ANNO
D HORMONE PRECURSOR (
                                                                                                                                                                               115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                               25
31
115
P
12852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE UPDATE)
ANNOTATION UPDATE)
SOR (PARATHYRIN) (PTH).
                                                         Score 35; DB 1; Length 115; Pred. No. 5.84e+00; 0; Mismatches 0; Indels
                                                                                                                                                                               PARATHYROID HORMONE; 98B67F47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COHN D.V.;
                                                            <u>;</u>
                                                            Gaps
                                                            0
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ID PHY CANPA
AC P52212.

ID PHY CANPA
AC P52212.

DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).

OC CAUSE FAMILIARIS (DOG).

OC CHICAROVORA.

RN [1]

OC CHICAROVORA.

RN [1]

SEQUENCE FROM N.A.
RC TISSUE-PARATHYROID,
RN [1]

RN [1]

BOUR LOT. J. STINNEYER C.L., MCCAULEY L.K., GRONE A.,
RC TISSUE-PARATHYROID;

RN ROSOLT J. STINNEYER C.L., MCCAULEY L.K., GRONE A.,
RC TISSUE-PARATHYROID;
1. FUNCTION: PTH ELEVATISS CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

DA ROSOLT J. STINNEYER S. CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

DE MEDL, U15662; 6559916; -..

FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

DE MEDL, U15662; 6559916; -..

FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

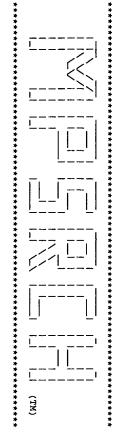
1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION: PTH ELEVATISE CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE 160:241-243(1995).

1. FUNCTION:
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:06:08 1998; MasPar time 3.81 Seconds 66.309 Million cell updates/sec

bular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-5 (1-6) from US08817547A.pep 35 1 SVSEIQ 6

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1.sp_fung1 2.sp_human 3.sp_invertebrate 4.sp_mammal
5.sp_mhc 6.sp_organelle 7.sp_phage 8.sp_plant
9.sp_bacteria 10.sp_rodent 11.sp_virus 12.sp_vertebrate
13.sp_unclassified

Statistics: Mean 17.730; Variance 12.970; scale 1.367

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query Match	Length	DB.	ID	Description	Pred. No.
ب	35	100.0	714	10	P70593	A-KINASE ANCHORING PRO	8.71e+00
2	35	100.0	771	w	Q20026	CODED FOR BY C. ELEGAN	8.71e+00
ω	ω S	94.3	315	ဖ	029062	3-HYDROXYACYL-COA DEHY	
4	ω w	94.3	324	ø	007213	HYPOTHETICAL 35.5 KD P	3.59e+01
5	ω	94.3	424	N	Q15916	ZID, ZINC FINGER PROTE	3.59e+01
0	ω	94.3	484	w	018032	TOSFIA.4.	3.59e+01
7	ω S	94.3	794	4	018742	LU-ECAM-1.	3.59e+01
8	33	94.3	801	N	Q13436	NUCLEOLAR RNA HELICASE	3.59e+01
9	33	94.3	820	4	018743	LU-ECAM-1.	3.59e+01
10	33	94.3	896	ø	Q55544	HYPOTHETICAL 100.3 KD	3.59e+01
11	33	94.3	905	4	018741	LU-ECAM-1.	3.59e+01
12	33	94.3	1967	11	010378	LARGE PROTEIN.	3.59e+01
13	32	91.4	43	N	Q14359	GALACTOSE-1-PHOSPHATE	7.10e+01
14	32	91.4	91	9	P72152	FLAG.	7.10e+01
15	32	91.4	131	11	P87572	E4 ORF1.	7.10e+01
16	32	91.4	239	9	P74971	PV. VESICATORIA ORF1.	7.10e+01
17	32	91.4	258	9	Q52785	ABC-TYPE PERMEASE HOMO	7.10e+01
18	32	91.4	270	9	Q53342	ORF 5' OF RPON.	7.10e+01
19	32	91.4	317	11	Q66606	VIRAL NUCLEOPROTEIN.	7.10e+01
20	32	91.4	329	9	026918	CONSERVED PROTEIN.	7.10e+01

444	42	41	40	39	38	37	36	3 5	34	ω ω	32	3 <u>1</u>	30	29	28	27	26	25	24	23	22	21
322	3 2	31	31	31	31	31	3	3 1	31	31	31	31	31	31	31	31	31	32	32	32	32	32
888.6	. 80	œ	8	œ.	.8			œ.	φ.	œ.	8	8		œ	8	8		۲.	91.4	91.4	91.4	91.4
1277 1277 1819	1106				764		471					298				146			679		595	466
ω N ω	N	1	\vdash	œ	œ	10	4	10	ø	Ø	9	9	N	9	ω	9	10	9	œ	ø	۳	2
098902 016625	015034	036363	Q06078	022113	P93756	Q61468	P79386	P97855	Q51919	Q47701	P71859	P74465	Q14538	007802	Q26980	Q55737	Q63473	Q44909	Q39603	Q44759	014301	Q13283
CODED FOR BY C. ELEGAN NEURAL CELL ADHESION M K10G6.3 PROTEIN.	318 (FRAGME	YME	SIMILAR TO TRANSCRIPTI	HCR2.	RECEPTOR-LIKE PROTEIN	MEGAKARYOCYTE POTENTIA	ORPHAN NUCLEAR RECEPTO	RAS-GTPASE-ACTIVATING	PUTATIVE CHAPERONINE (POLYSACCHARIDE CHAIN L	HYPOTHETICAL 33.9 KD P	PILIN BIOGENESIS PROTE	MACROPHAGE LECTIN 2.	HYPOTHETICAL 27.4 KD P	ZEN TC (FRAGMENT).	, 16.4 KD	PARATHYROID HORMONE (F	FLAGELLAR EXPORT PROTE	HEAT SHOCK PROTEIN 70B	FLHA.	BETA-TRANSDUCIN.	GAP SH3 BINDING PROTEI
1.37e+02 1.37e+02 1.37e+02		•	1.37e+02	٠.	1.37e+02						1.37e+02	1.37e+02		1.37e+02	1.37e+02				7.10e+01	7.10e+01	7.10e+01	7.10e+01

RA RA	ROSSETT	Qy RESULT	* # # O	RAP RR	RESULT AC DT ODT ODT OC OC E
SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 94150718. MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,	01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) CODED FOR BY C. ELEGANS CDNA CEESB82F. F35C8.7. F35C8.7. CAENORHABDITIS ELEGANS. EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.	1	⊢		TT 1 P70593 PRELIMINARY; PRT; 714 AA. P70593; 01-FEB-1997 (TREMBLREL. 02, CREATED) 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE) 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE) A-KINASE ANCHORING PROTEIN AKAP150. RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

```
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., RA PARSONS J., PERCY C., RIFKEN L., ROODRA A., SAUNDERS D., SHOMNKEEN R., RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WORTERSTON R., RI NATURE 368:32-38(1994).

RN [2]
RN [2]
RN [2]
RN SEQUENCE FROM N.A.
RN [3]
RN SEQUENCE FROM N.A.
RN SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SEQUENCE FROM N.A.
RN SEQUENCE
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10 28 10 10 11 11 11 11 11 11 11 11 11 11 11	e de	Database: Statistics:	<pre>uence: ring table: rched: t-processing:</pre>	Relea Copyr p pro output	
100.0 16 25 W21948 Fusion protein compri 7.96e+02 100.0 20 25 W21947 Fusion protein compri 7.96e+02 100.0 34 4 R22299 Human parathyroid hor 7.96e+02 100.0 34 22 W19994 Cyvlised human parath 7.96e+02 100.0 34 22 W17967 Human PTH analogue [C 7.96e+02 100.0 34 22 W17960 Human PTH analogue [C 7.96e+02 100.0 34 9 R58218 [L8,A16,O18,A19,T33,A 7.96e+02 100.0 34 9 R58218 [L8,A16,O18,A19,T33,A 7.96e+02 100.0 34 8 R41578 [Lys14,J5,16,L7]hPFH 7.96e+02 100.0 34 7 R3453 Human parathyroid hor 7.96e+02 100.0 34 7 R3453 Human parathyroid hor 7.96e+02 100.0 34 22 W17948 Human parathyroid hor 7.96e+02 100.0 34 22 W17948 Human parathyroid hor 7.96e+02 100.0 34 22 W17948 Human parathyroid hor 7.96e+02 100.0 35 5 F10110 Human parathyroid hor 7.96e+02 100.0 35 14 R74415 Parathyroid hormone p 7.96e+02 Parathyroid horm	is the number of results predicted by chance to have a ster than or equal to the score of the result being privaled by analysis of the total score distribution. SUMMARIES SUMMARIES B Ourry Description Precedents Precedents Precedents Precedents Precedents B Description Precedents Precedents	a-geneseq31-2 l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 l:part1 2:part2 3:part10 11:part11 12:part12 13:part13 l4:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 Mean 11.317; Variance 26.409; scale 0.429	בא ה טם ד	.1A John F. Collins, Blocomputing Research Unit. (c) 1993-1998 University of Edinburgh, U.K. istribution rights by Oxford Molecular Ltd - protein database search, using Smith-Waterman algorithm u Jul 30 10:09:42 1998; MasPar time 2.61 Seconds 29.338 Million cell updates/sec generated. 29.338 Million cell updates/sec from US08817547A.pep	

	44444888888888888888888888888888888888
	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
	11111111111111111111111111111111111111
	222 2222 2222 2222 2222 2222 2222 2222 2222
ALIGNMENTS	R58227 R582284 R58284 R58284 R58298 R58298 R58298 R58298 R58298 R58298 R58298 R5829
	[D-Gln29]-hPTH(1-36)-Ser-Val-(hPTH 3-35)-P [D-Gln6]-hPTH(1-36)-N [D-Gln6]-hPTH(1-36)-N [D-Gln6]-hPTH(1-36)-N [D-Gln6]-hPTH(1-36)-N [D-Gln6]-hPTH(1-36)-N [D-Gln6]-hPTH(1-38)-N [
	7.96e+02 7.96e+02

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The rankly rold hormone production

The DNA encoding the present sequence, a linker and residues 1-7 of the DNA encoding the present sequence, a linker and residues 1-7 of the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII (SA) sequence, to give psA-TFV-PTH. psA-TFV-PTH and the LacIq repressor plasmid pUBS500 were used to transform E. coli K12 RM82.

The transformants were grown, with IPTG induction, in medium containing kanamycin and amplicilin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidine hydrochloride, and renatured by dilution in pH 7 phosphate buffer. The solution was clarified and the supernatant concentrated and countified on a column of immobilised iminobiotin. The purified contactial was incubated with tobacco etch virus (TEV) NIA protease conditions are not released, recovered by SA fragment concentrated.
                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1997.
06-NOV-1996;
16-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W21948 standard; Protein; 16 AA.
W21948;
30-JAN-1998 (first entry)
Fusion protein comprising linker and PTH 1-37 (residues 1-7).
Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin;
fusion protein; recombinant production; TEV NIa protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                         Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and
                                                                                                                                                                                                                                                                                                                                                                (BOEF ) BOEHRINGER MANNHEIM GMBH KOPEtzki E; WPI; 97-289290/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                               N-PSDB; T73912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9718314-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tobacco etch virus.
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DE-042702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "linker cleavable by TEV NIa protease" 10..16 /note= "parathyroid homone 1-27 /----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "parathyroid homone 1-37 (residues 1-7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Met(13-139) streptavidin residue"
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Search completed: Thu Job time: 16 secs.
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PT parathyroid hormone production
PT parath
                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;

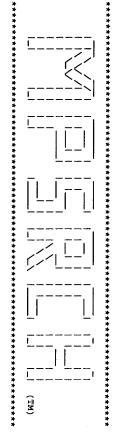
Best Local Similarity 100.0%;

Conservative
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22-MAY-1997.
06-NOV-1995; DE-042702.
(BOEF) BOEHRINGER MANNHEIM GMBH.
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|||||
1 SVSEI 5
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WPI; 97-289290/26.
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W21947 standard; Protein; 20
W21947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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               Jul 30 10:09:58 1998
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2.13
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                                                                                                                                                                                 Score 28; DB 25; Le
Pred. No. 7.96e+02;
0; Mismatches 0;
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Pred. No. 7.96e+02;
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MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:09:06 1998; MasPar time 2.97 Seconds 61.602 Million cell updates/sec

abular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-6 (1-5) from US08817547A.pep 28 1 SVSEI 5

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 16.244; Variance 13.192; scale 1.231

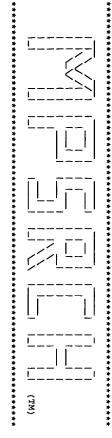
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NO.	Score	Query Match	Length	DB	Ħ	Description	z
ᆫ	28	100.0	34	5	1HTH	cyclic parathyroid ho	3.60e+02
N	28	•	34	u	1ZWA	yroid hormone	თ
ω	28	•	37	v	1HPH		3.60e+02
4	28		115	ν	JC4202		3.60e+02
ហ	28	100.0	126	N	S75413	hypothetical protein	
5	28		227	N	S54466	Н	•
7	28	•	303	N	A64150	Н	٠
8	28	•	308	N	JQ1401	glutathione synthase	.60e+0
9	28	•	316	G	10NRA	transaldolase b (EC 2	.60e+0
10	28	100.0	316	U	10NRB	transaldolase b (EC 2	.60e+0
11	28	•	316	G	1UCWA	transaldolase (EC 2.2	.60e+0
12	28	100.0	316	u	1UCWB	(EC 2	3.60e+02
13	28		344	N	A30544	dnaK-type molecular c	.60e+0
14	28	100.0	362	2	S12895	polygalacturonase (EC	
15	28	•	387	N	S33517	tubulin alpha chain -	
16	28	•	389	Ν	S20933	naringenin-chalcone s	
17	28	100.0	389	N	S33610	naringenin-chalcone s	
18	28	100.0	389	N	S35167	naringenin-chalcone s	
19	28	100.0	389	N	S26414	naringenin-chalcone s	
20	28		405	N	A35620	coenzyme F420 hydroge	
21	28		408	N	A69040	F420-	
22	28	100.0	415	ν	S63221	DNA-directed RNA poly	
23	28	100.0	420	N	C64552	VII,	3.60e+02

4.4	4 3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0							100.0	100.0
2844	1232	1146	1116	1039	974	962	921	915	853	741	737	691	628	609	609	491	458	453	451	450
2	ง	N	N	N	N	N	N	N	N	Ν	N	N	N	N	N	N	N	N	N	N
S28291	B39432	S07915	S41915	S02711	A44484	S58107	A55854	A43802	S34682	S50340	S63453	S54262	A69381	S29698	S55957	в69499	S44741	S07459	JC4133	A45547
hypothetical protein	ndent de	RF2 protein - yeast (DNA-directed RNA poly	ω	:3	hypothetical protein	secA protein - Caulob	cellulase (EC 3.2.1.4	probable transport pr	CHL12 protein - yeast	probable RNA helicase	/l-accepting	type II secretion sys	dnaK-type molecular c	hypothetical protein	sodium- and chloride-	C02C2.3 protein - Cae	tubulin alpha-I chain	alpha-tubulin isoform	tubulin alpha-II chai
3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02

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FEATURE FRESTON Heltx (right hand alpha) (193-10 strepton heltx (right hand alpha) (193-10 strepton heltx (right hand alpha) (193-10 strepton heltx (right hand alpha) (193-10 strength 34; Bert Local Samilarity 100.0%; Secaré No. 3 Sou-Op; Longth 34; Bert Local Samilarity 100.0%; Pred. No. 3 Sou-Op; Longth 34; Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0; 19:1111 (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (193-11) (1
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:07:59 1998; MasPar time 2.00 Seconds 62.621 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-6 (1-5) from US08817547A.pep 28

1 SVSEI 5

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 16.927; Variance 10.693; scale 1.583

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 28 100.0 2 28 100.0 3 28 100.0 4 28 100.0 5 28 100.0 6 28 100.0 7 28 100.0 9 28 100.0 10 28 100.0 11 28 100.0 11 28 100.0 11 28 100.0 12 28 100.0 13 28 100.0 14 28 100.0 15 28 100.0 16 28 100.0 17 28 100.0	No. Score Match
93 1 115 1 115 1 115 1 117 1 1 1 1	Length DB
TRBJ_ECOLI PTHY_HUMAN PTHY_HUMAN PTHY_PIG TBA_PLAYO TBAA_PLAYO TBAA_PLAYO TBAA_PLAYO TBAA_BCHCOLI TBAA_BCHCOLI TBAA_BCHCOLI TBAA_BCHCOLI TBAA_BCHCOLI TBAA_BCHCOLI TBAA_BCHCOLI CHS3_TRISO CHS3_MEDSA CHS3_MEDSA CHS3_MEDSA CHS3_PEA CHS3_PEA CHS3_PEA CHS3_PEA CHS3_PEA CHS3_MEDSA	ID
TRBJ PROTEIN. PARATHYROID HORMONE PR POUBLIN ALPHA CHAIN (F PHYPOTHETICAL 24.9 KD P HYPOTHETICAL PROTEIN H PRANSALOLLASE B (EC 2. TUBULIN ALPHA-8 CHAIN POLYGALACTURONASE II P POLYGALACTURONASE II P POLYGALACTURONASE II P CHALCONE SYNTHASE 4 (E CHALCONE SYNTHASE 4-1 CHALCONE SYNTHASE 17 (ECHALCONE SYNTHASE 17 (ECHALCONE SYNTHASE 17 (ECHALCONE SYNTHASE 18 (ECHALCONE SYNTHASE 18 (ECHALCONE SYNTHASE 19 (ECHALCONE	Description
1.27e+02 1.27e+02	Pred. No.

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24
28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
2916	1505	1332	1146	1116	1039	974	962	921	737	644	621	609	609	493	458	453	451	451	448	447	445
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YN81_CAEEL	CDP_HUMAN	CDP_MOUSE	KTXA_KLULA	RPOB_HETCA	GUNB_CALSA	SIN4_YEAST	YA4E_SCHPO	SECA_CAUCR	SUV3_YEAST	KNH_HUMAN	DNAK_MYCLE	DNAK_MYCTU	YL01_YEAST	PUR1_SYNP7	YKH3_CAEEL	TBA_PLAFK	TBA_TRYBR	TBA_TORMA	TBA_CANAL	TBA1_YEAST	TBA3_YEAST
HYPOTHETICAL 316.1 KD	CCAAT DISPLACEMENT PRO	CCAAT DISPLACEMENT PRO	KILLER TOXIN ALPHA AND	DNA-DIRECTED RNA POLYM	ENDOGLUCANASE B PRECUR	GLOBAL TRANSCRIPTIONAL	HYPOTHETICAL TRP-ASP R	PREPROTEIN TRANSLOCASE	MITOCHONDRIAL ATP-DEPE	KININOGEN, HMW PRECURS	DNAK PROTEIN (HEAT SHO	DNAK PROTEIN.	HYPOTHETICAL 69.8 KD P	AMIDOPHOSPHORIBOSYLTRA	HYPOTHETICAL ACETYLCHO	TUBULIN ALPHA CHAIN.	TUBULIN ALPHA CHAIN.	TUBULIN ALPHA CHAIN (A	TUBULIN ALPHA CHAIN.	TUBULIN ALPHA-1 CHAIN.	TUBULIN ALPHA-3 CHAIN.
1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02

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GR D D D A	RESULT	Qy	ğ	Ma Ma	SQ	XΨ	DR S	g 5	88	23	Z :	R R	R	RL	Š	₹ :	ദ്	g 5	8	గ	ដ	ö	z i	7 1	3 5	H	AC	RESULT	
01-OCT-1996 (REL. 34, CREATED) 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH). PTH.	LT 2 PTHY CANFA STANDARD; PRT; 115 AA.	1 SVSEI	66 SVSEI 70	100.0%; Score 28; DB 1; Length 93; Best Local Similarity 100.0%; Pred. No. 1.27e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 93 AA; 10160 MW; C604F894 CRC32;		PIR; F32238; QQEC25.	MO1150: G308535: -	ON: UNKNOWN.	BIOL. REV. 58:162-210(1994).	S. IPPEN-THLER	SEQUENCE FROM N.A. MEDLINE: 94359430.		BACTERIOL. 171:21:	IPPEN-IHLER K	MEDLINE; 89123020.	_	SEOUENCE FROM N.A.	ENTEROBACTERIACEAE.	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;		ESCHERICHIA COLI.	TRBJ.	(1000. 047 000	O1-009-1996 (RET. 34, LAST ANNOTATION HEDATE)	(REL. 16, CREATED)	P18353;	LT 1 TRBJ_ECOLI STANDARD; PRT; 93 AA.	

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Search completed: Thu Jul 30 10:08:06 1998 Job time: 7 secs.
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                                                                                                                B
                                                                                                                                                                                                                             RC TISSUE-PARATHYROID;

RC TISSUE-PARATHYROID;

RX MEDLINE; 9536665C;

RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

RA ROSOL T.J., STEINMEYER C.L.,

GENE 160:241-243(1995).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

BONE AND PREVENTING THEIR RENAL EXCRETION.

BORE AND PROVENTING THEIR RENAL EXCRETION.

BORE MADI, U15662, G558916; --

BORE MONE; STEINAL.

FT FOROTE; PS00335; PARATHYROID; 1.

KW HORMONE; SIGNAL.

PT SIGNAL.

25

BY SIMILARITY.

FT FOROTE 26

31

BY SIMILARITY.

FT FOROTE 26

31

BY SIMILARITY.

FT FOROTE 26

31

BY SIMILARITY.

FT CHAIN

32

115

PARATHYROID HORMONE.

SQ SEQUENCE 115 AA; 12957 MW; 16EDOEBC CRC32;
                                                                                                                                          uery Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANIS FAMILIARIS (DOG).
EURARYOTA; METAAOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CARNIVORA.
[1]
                                                                         32 SVSEI 36
|||||
1 SVSEI 5
                                                                                                                                Score 28; DB 1; Length 115;
Pred. No. 1.27e+02;
0; Mismatches 0; Indels
                                                                                                                                  0;
                                                                                                                                  Gaps
                                                                                                                                0,
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1 28 28 8 8 8 7 28 8 8 8 8 8 8 11 11 11 11 11 11 11 11 11			Database:	Post-processing:	Scoring table Searched:	Title: Description: Perfect Score Sequence:	on:	rch_pp	
100.0 82 100.0 113 100.0 126 100.0 228 100.0 228 100.0 250 100.0 338 100.0 379 100.0 378 100.0 389 100.0 389 100.0 389 100.0 389 100.0 425	rived by % Query Query Lei	6.468 numbe	sptremb15 1:sp_fung 5:sp_mhc 9:sp_bact 13:sp_unc	ng: Minimum Match Listing first	: PAM 150 Gap 15 140542 seqs	>US-08-817- (1-5) from : 28 1 SVSEI 5	Thu Jul	ease 3.1A John yright (c) 199 Distribut	
9 030721 9 0316290 9 051810 9 051810 9 P95985 2 015631 10 P97891 10 P97891 10 028438 9 028438 9 0244791 9 0244791 9 0248388 9 023888 8 023888 8 023888 9 024888 9 024888 9 024888 9 024888 9 024888 9 024888 9 024888 9 024888	of the SUMMARI	; Variance r of results equal to the	l5 _fungi 2:sp_human 3: _mhc 6:sp_organelle _bacteria 10:sp_rode _unclassified	ch 0% st 45 summaries	, 42109429 r	547A-6 US08817547A.pep	0:08:23 1998;	. Collins, B 1998 Univer n rights by	
HYPOTHETICAL 9.0 KD PR F32D1.8 PROTEIN. HYPOTHETICAL 12.6 KD P ORF C04047. F1589.1. TRANSLIN. TRANSLIN. TRANSLIN. PKSB. METHIONYL AMINOPEPTIDA ERPD. PLASMID PMCCC7 MCCA, B, ALPHA-TUBULIN (FRAGMEN ERPJ. CHALCONE SYNTHASE (EC CHALCONE SYNTHASE (EC 1-AMINOCYCLOPROPANE 1- EXONUCLEASE VII, LARGE ALPHA-TUBULIN.	score distributio	714; scale 1.537 edicted by chance to have on the result being	sp_invertebrate 4:sp_ma 7:sp_phage 8:sp_plant nt 11:sp_virus 12:sp_ve	ŭ	esidues	Ü	MasPar time 3.56 Sec 59.081 Million cell	computing Research Unit ty of Edinburgh, U.K. ford Molecular Ltd	
1.95e+02 1.95e+02	Pred. No.	/e a printed,	ammal ertebrate				tes/se	algorith	* * * * * * * * * * * * * * * * *

45	44	٠ ۵ د	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28	27	26	25	24	23	22	21
28	28	2 6	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
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014029	P70298	022342	014529	008994	Q24212	P97527	014148	013690	Q20026	013479	Q53171	004561	Q45192	029213	006301	P93718	P93719	Q19971	028284	Q96579	Q43810	Q94572	Q27352	Q25790
ICA	E 2 (CUX-2).	٠, ۲	ω ~ 1	CUX/CDP (FRAGMENT).	STN-B.	NB-2.	HYPOTHETICAL HELICASE		CODED FOR BY C. ELEGAN	SECRETED DIPEPTIDYL PE	PR	٠	(PBR STRAIN) P83/100 G	TYPE II SECRETION SYST	DNAK.	PETHY, ZPT4-2.	TRANSCRIPTION FACTOR 2	COSMID F32E10.	SODIUM- AND CHLORIDE-D	1-AMINOCYCLOPROPANE-1-	CLOPROPANE	ALPHA-III TUBULIN.	ALPHA TUBULIN.	ALPHA-TUBULIN II.
.95e+0	5e+0	956+0	95e+0	.95e+0	.95e+0	1.95e+02	1.95e+02	.95e+0	1.95e+02	1.95e+02	÷	1.95e+02	1.95e+02	٠,	1.95e+02	٠,	1.95e+02	1.95e+02	1.95e+02	1.95e+02	1.95e+02	1.95e+02	1.95e+02	'n

ALIGNMENTS

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RESULT 2

O16290;
AC 016290;
DT 01-CAN-1998 (TREMBLREL 05, CREATED)
DT 01-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
DT 01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
DE F32D1.8 PROTEIN.
GN F32D1.8 CAEMORHABDITIS ELEGANS.
CAEMORHABDITIS ELEGANS.
CC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
1 O30721;
AC O30721;
DT O1-JAN-1998 (TREMBLREL. 05, CREATED)
DT O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT O1-JAN-1998 (TREMBLREL. 05, LAST ANNOYATION UPDATE)
DT HYPOTHETICAL 9, OKD PROTEIN (FRAKMENT).
OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERLA;
OC AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN-CCUG 17874;
RA MASIGNANI V., ARICO' B.;
RA MASIGNANI V., ARICO', B.;
RA MASIGNANI V., ARICO', B.;
RM SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AFO16039; G2367603; -.
KW HYPOTHETICAL PROTEIN.
FT NON_TER 82
SQ SEQUENCE 82 AA; 9025 MW; 25304A67 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CCUG 17874;
MASIGNANU V., ARICO' B.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (SP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
HYPOTHETICAL PROTEIN.
NON_TER
82
82
SEQUENCE 82 AA; 9025 MW; 25304A67 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 SVSEI 10
|||||
1 SVSEI 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 9; Length 82; Pred. No. 1.95e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXYON M., DERAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWELS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LATSTER N., LATERILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SUUNDERS D., SHOWNKEEN R.,
RA HISTON A., WEINSTOCK L., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RL NATURE 568:22-38(1994).
RE SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RI SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SITAIN-BRISTOL N2;
RA SITAIN-BRISTOL N2;
RA SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA SEQUENCE FROM N.A.
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RMATERSTON R.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, APO16427; GZ291235; -
EMBL, APO16427; GZ291235; -
EMBL, APO16427; GZ291235; -
BEST LOCAL SIMILARITY 100.0%; SCOIC 28; DB 3; Length 110;
BEST LOCAL SIMILARITY 100.0%; SCOIC 28; DB 3; Length 110;
BEST LOCAL SIMILARITY 100.0%; PPEGL NO. 1.95e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 36 SVSEI 40

10 1111

Qy 1 SVSEI 5

Search completed: Thu Jul 30 10:08:48 1998

Search completed: Thu Jul 30 10:08:48 1998
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***	(TM)	****

MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:12:14 1998;

Pabular output not generated. MasPar time 2.65 Seconds 57.826 Million cell updates/sec

Title: >US-08-817-547A-7 (1-10) from US08817547A.pep 73

Description: Perfect Score:

Sequence: 1 HNLGKHLNSM 10

Scoring table: PAM 150 Gap 15 Gap

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.178; Variance 63.374; scale 0.255

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	Query Match L	Length	BB	ID	Description	Pred. No.
1	73	100.0	28	4	R22064	Modified hPTH(7-34)NH	1.59e+00
2	73	100.0	34	14	R74521	Human parathyroid hor	1.59e+00
ω	73	100.0	34	22	W17957	Human parathyroid hor	1.59e+00
4	73	100.0		22	W17954		1.59e+00
ហ	73	100.0	34	22	W17968	•	1.59e+00
თ	73	100.0		22	W17950	Œ	1.59e+00
7	73	100.0		22	W17969	Human parathyroid hor	1.59e+00
&	73	100.0		22	W17951	Human parathyroid hor	1.59e+00
9	73	100.0		10	R55724	Parathormone N-termin	1.59e+00
10	73	100.0		7	R34457	Human parathyroid hor	1.59e+00
11	73	100.0	34	7	R34364	Human parathyroid hor	1.59e+00
12	73	100.0	34	19	R98951	Target peptide (PTH(1	1.59e+00
13	73	100.0	34	7	R34363	О	1.59e+00
14	73	100.0		22	W17955	Human parathyroid hor	1.59e+00
15	73	100.0		22	W17947	Human parathyroid hor	1.59e+00
16	73	100.0		22	W20000	Cyclised human parath	1.59e+00
17	73	100.0	36	9	R58290	[Ala26]-hPTH(1-36)-NH	1.59e+00
18	73	100.0	36	φ	R58295	[D-Val35]-hPTH(1-36)-	1.59e+00
19	73	100.0	36	9	R58175	[Pyridine-2-carboxyli	1.59e+00

Query Match 100.0%; Best Local Similarity 100.0%; Matches 10; Conservative

Score 73; DB 4; Ler Pred. No. 1.59e+00; 0; Mismatches 0;

Length 28; Indels

0

Gaps

0;

73 100.0 36 9 R58252 [Asn]]-PbTH(1-36)-NH2 73 100.0 36 9 R58263 [D-11e5]-PbTH(1-36)-NH2 73 100.0 36 9 R58263 [D-11e5]-PbTH(1-36)-NH2 73 100.0 36 9 R58268 [Cha8]-PbTH(1-36)-NH2 73 100.0 36 9 R58297 [Pro35]-PbTH(1-36)-NH2 73 100.0 36 9 R58297 [Pro35]-PbTH(1-36)-OH. 73 100.0 38 9 R58029 [D-Leul]-PbTH(1-38)-OH. 73 100.0 38 9 R58152 [Arg22]-PbTH(1-38)-OH. 73 100.0 38 9 R58154 [Arg22]-PbTH(1-38)-OH. 73 100.0 38 9 R58159 [Hisl]-PbTH(1-38)-OH. 73 100.0 38 9 R58159 [Hisl]-PbTH(1-38)-OH. 73 100.0 38 9 R58129 [Hisl]-PbTH(1-38)-OH. 73 100.0 44 26 P30015 Human parathyroid hor. 73 100.0 47 25 W21946 Fusion protien comprision of the comprision of th	45	44	43	42	41	40	39	38	37	36	35 5	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20
36 9 R58252 36 9 R58253 36 9 R58253 37	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	/3
9 R58253 [4-aminopenizole at 9 R58252 [4-sn]]-hpTH(1-36) 9 R58263 [D-11e5]-hpTH(1-36) 9 R58268 [Cha8]-hpTH(1-36) 9 R58267 [P-035]-hpTH(1-36) 9 R58277 [D-Leul]]-hpTH(1-38) 9 R58278 [Aug22]-hpTH(1-38) 9 R58152 [Aug22]-hpTH(1-38) 9 R58152 [Aug22]-hpTH(1-38) 9 R58152 [Aug22]-hpTH(1-38) 9 R58152 [Aug22]-hpTH(1-38) 9 R58132 [Pro19]-hpTH(1-38) 9 R58132 [Pro19]-hpTH(1-38) 9 R58132 [Pro19]-hpTH(1-38) 9 R58132 [Pro19]-hpTH(1-38) 10 R58132 [Pro19]-hpTH(1-38) 11 R758132 [Pro19]-hpTH(1-38) 12 R58132 [Pro19]-hpTH(1-38) 13 R758132 [Pro19]-hpTH(1-38) 14 R21139 [Pro19]-hpTH(1-38) 15 R721189 [Pro19]-hpTH(1-38) 16 R21189 [Pro19]-hpTH(1-38) 17 W25687 [Pro19]-hpTH(1-38) 18 R21189 [Pro19]-hpTH(1-38)	•	•	•	٠	•	•	•	•	•	•	•		•	•	•	•	•	•		•	•	•	•	٠	•	٠
9 R58253 [4-smillopenzolc at 9 R58253 [Asni]-hpFH(1-36) 9 R58268 [Cha8]-hpFH(1-36) 9 R58268 [Cha8]-hpFH(1-36) 9 R58268 [Cha8]-hpFH(1-36) 9 R58270 [D-Leuil]-hpFH(1-38) 9 R58152 [Arg22]-hpFH(1-38) 9 R58152 [Arg22]-hpFH(1-38) 9 R58152 [Arg22]-hpFH(1-38) 9 R58152 [Arg22]-hpFH(1-38) 9 R58132 [Arg22]-hpFH(1-38) 9 R58132 [Human parathyroid 5 W21946 Fusion protien con 6 R30853 Human parathyroid 4 R21190 Human parathyroid 4 R21191 Human parathyroid 4 R21189 Human parathyroid 4 R21189 Human parathyroid 4 R21189 Human parathyroid 6 R30853 Human parathyroid 7 R2189 Human parathyroid 8 R2188 Human parathyroid 8 R2188 Human parathyroid 8 R23338 Human parathyroid 9 Human 9	115	84	84	84	84	84	84	84	84	84	79	47	44	38	38	38	38	38	38	38	36	36	36	36	36	u
52 [A=nnInopenzoic ac [4-annInopenzoic] ac [4-annIn	13	4	25	4	4	4	4	4	4	27	σ	25	26	9			φ	9	ဖ	φ	φ	ø	ø	ဖ	9	ď
minopenzoic a hpTH(1-36) le5 -hpTH(1-36) hpTH(1-36) hpTH(1-	56	323	942	118	118	R21192	11	R21190	119	568	280	194	001	813	812	895	815	815	814	802	827	829	826	826	825	272
	_	parathyroid	parathyroid	n parathyroid	parathyroid	parathyroid	n parathyroid	parathyroid	parathyroid	parathyroid	utein lacking	protien con	parathyroid]-hPTH(1-38))-hPTH(1-38)	peptide (F	2]-hPTH(1-38)	2]-hPTH(1-38)-]-hPTH(1-38)-	ul]-hPTH(1-38	Leull]-hPTH(1-36	-hPTH(1-36)	-hPTH(1-36)-]-hPTH(1-36)-]-hPTH(1-36)-NH	ac

```
we parathyroid hormone analogues - useful for treatment and in vitro diagnosis of PTH-dependent tumours, immune disorders, osteoporosis and hyperparathyroidism.

So claim 1; Column 10; 6pp; English.

The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N.N-diisobutyl or 3-phenylpropancyl. The PTH canalogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bioactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bioassays to measure naturally occurring PTH and to diagnose the etiology of or to treat hyperthyroidism and diseases caused by abberrent prodn. of hormone-like substances, such as tumours. It may also be used to treat hyperthyroidism and diseases caused by abberrent prodn. of phase synthesis.

See also R22058-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Key
modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R22064;
14-JUL-1992 (first entry)
Modified hPTH(7-34)NH2.
Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
tumours; hypercalcaemia; renal failure; human.
                                                                                                                                                                                                                                                                                                         03-MAR-1992.
25-APR-1990; US-514394.
25-APR-1990; US-514394.
25-APR-1990; US-514394.
(MERI ) MERCK & CO INC.
ROSENDIATT M, ROUDINI E, Chorev M, Nutt RF;
ROSENDIATT M, ROUDINI E, Chorev M, Nutt RF;
WPI; 92-096233/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R22064 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                             US5093233-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                               28
/label= NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= OTHER
/note= "OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
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RESULT ID R7
                                                                                                                                                                                                               pp 04-MAY-1995.

PF 25-OCT-1993; US-142551.

(AFFY-) AFFYMAX TECHNOLOGIES NV.

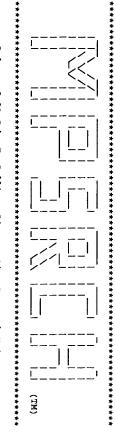
Oldenburg KR, Selick HE;

DR WPI; 95-17880/23.

PT New active analogues of parathyroid hormone - with increased extivity, stability in serum etc., esp. for treating osteoporosis, also related DNA and vectors

PS Disclosure; Page 1; 109pp; English.

CC This sequence represents residues 1-34 of human parathyroid hormone (RPTH). This sequence was used in the production of analogues of the CC truncated form of prH. These analogues have increased activity and CC longer serum half life than native PTH due to eg. substitution of Met CC carboxy terminal may also be modified by the addition of a homoserine CC residue or analogue, or by the addition of residues 35-84 of wild type CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic have increased iontophoretic transdermal transport compared to wild type Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  망
                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
arch completed: Thu Jul 30 10:12:36 1998 time : 22 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R74521 standard; Peptide; 34 AA.
R74521;
04-DEC-1995 (first entry)
04-DEC-1995 (first entry)
Human parathyroid hormone (1-34).
Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution; metabolic bone disease; human; veterinary medicine; iontophoretic transdermal transport; recombinant E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9511988-A.
                                                                                         9 hnlgkhlnsm 18
                                                                       HNLGKHLNSM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 hnlgkhlnsm 12
||||||||
1 HNLGKHLNSM 10
                                                                                                                             Score 73; DB 14; Length 34;
Pred. No. 1.59e+00;
0; Mismatches 0; Indels
                                                                                                                                0;
                                                                                                                           Gaps
                                                                                                                           0
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:11:22 1998; MasPar time 3.20 Seconds 114.268 Million cell updates/sec

abular output not generated.

Title: >US-08-817-547A-7
Description: (1-10) from US08817547A.pep
Perfect Score: 73

Sequence: 1 HNLGKHLNSM 10

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 22.338; Variance 29.941; scale 0.746

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22211154 2221216 2221216	NO.
4444445555566667337733 444448669957337733773	Score
100.0 100.0	% Query Match
34 34 34 35 35 37 37 37 37 37 37 37 37 37 37 37 37 37	Length
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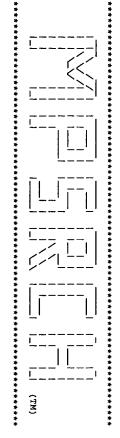
45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
45	45	45	45	45	<u>4</u> 5	46	46	46	46	46	46	46	40	46	46	46	46	46	47	47	47
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985	885	700	443	405	186	2068	1708	1490	1447	827	568	418	417	417	417	193	176	152	744	738	621
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S59330	VCPVF2	S12053	E65008	A41252	A64646	A47371	F69189	S32373	S63669	S25949	S76244	I52968	A42843	S20608	A40968	A53835	S22310	S22311	A32905	S35093	S35092
Na+/H+-exchanging pro	structural protein OR	protein-tyrosine-phos	hypothetical protein	otein 4	site-specific recombi	transcription initiat	magnesium chelatase s	DNA-binding protein T	UDPglucoseglycoprot	gene coxII intron 2 p	hypothetical protein	colligin-2 - human		heat shock protein Hs	heat shock protein 47	SEC63 protein complex	HMG-Y-related protein	HMG-Y-related protein	` Q	plakoglobin - African	plakoglobin – mouse (
				5.57e+01	5.57e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01		3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	2.40e+01	2.40e+01	2.40e+01

RESULT 2 ENTRY TITLE parathyroid ALTERNATE NAMES HPTH(4-37) PDB_TITLE structure of structures ORGANISM #formal_name REFERENCE A07860 #authors Roesch, P.; #submission submitted to #cross-references PDB:1ZWE REFERENCE TN001721 #authors in Strukture pp.0, Bayr	Query Match Best Local Similar Matches 10; Co Db 9 HNLGKHLNSM	0 0	REFERENCE TN001717 #authors Marx, U.C. #book in Strukture #book pp.0, Bayr COMMENT Resolution: not app COMMENT Determination: NMR	ORGANISM REFERENCE #authors #submission	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
12WE #type complete parathyroid hormone (residues 4-37) - human HTPH(4-37) HTPH(4-37) Structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 Roessch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 pes PDB:12WE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	100.0 ity 100.0 nservativ 18	#region helix (right hand alpha)\ #region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629	TMO01717 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR	#formal_name Homo sapiens #common_name man A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996	12WA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10

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COMMENT Determination: not applicable
COMMENT Determination: NMR
EXPROPES hormone

15-25 #*eqion helix (right hand alpha)
SUMMARY Match 100.0%; Score 73; DB 5; Length 34;
Best Local Similarity 100.0%; Pred No. 7.13e-05; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 HNLGKHLNSH 15
Qy 1 HUJCHLMSH 10
Search completed: Thu Jul 30 10:11:56 1998
Job time: 34 Secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 10:10:15 1998; MasPar time 2.14 Seconds 117.135 Million cell updates/sec

on:

Title:
Description:
Perfect Score: >US-08-817-547A-7 (1-10) from US08817547A.pep 73

Sequence: 1 HNLGKHLNSM 10

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.362; Variance 25.262; scale 0.925

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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700	208	2068	418	417	417	417	192	176	152	743	738	621	187	887	381	171	115	115	115	115	115	Length
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47 KD HEAT SHOCK PROTE PROTEIN-TYROSINE PHOSP	σ	TRANSCRIPTION INITIATI	COLLAGEN-BINDING PROTE	47 KD HEAT SHOCK PROTE	47 KD HEAT SHOCK PROTE	47 KD HEAT SHOCK PROTE	TRANSLOCATION PROTEIN	HMG-Y RELATED PROTEIN	HMG-Y RELATED PROTEIN	JUNCTION PLAKOGLOBIN (JUNCTION PLAKOGLOBIN (JUNCTION PLAKOGLOBIN (ATP SYNTHASE DELTA CHA	26S PROTEASOME REGULAT	ESTRADIOL 17 BETA-DEHY	PROTEASE SYNTHASE AND	PARATHYROID HORMONE PR	Description				
1.69e+01 1.69e+01	1.69e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	6.28e+00	6.28e+00	6.28e+00	6.28e+00	3.78e+00		3.78e+00	8.86e-03	1.50e-03	1.99e-05	1.99e-05	1.53e-06	Pred. No.

45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	ω ω	32	31	30	29	28	27	26	25	24
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58.9	58.9	58.9	58.9	58.9	58.9	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3		60.3		•	61.6	•
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SP14_YEAST	YPT7_CAEEL	BICD_DROME	VP4_ROTHU	RADA_METJA	LDH_METJA	POLR_ASGVP	BIMC_EMENI	YG2K_YEAST	YQD3_CAEEL	YFC3_YEAST	Y187_MYCGE	HSF1_HUMAN	HSF1_MOUSE	VC17_VACCC	KSF1_ECOLI	HEMZ_BACSU	YHBV_ECOLI	APA1_PIG	PMGY_MYCLE	NAH_YEAST	NS2_SIDEV
PHOSPHOLIPASE D1 (EC 3	HYPOTHETICAL 111.7 KD	CYTOSKELETON-LIKE BICA	OUTER CAPSID PROTEIN V	RADA PROTEIN.	L-LACTATE DEHYDROGENAS	GENOME POLYPROTEIN (CN	KINESIN-LIKE PROTEIN B	HYPOTHETICAL 106.5 KD	HYPOTHETICAL 96.7 KD P	HYPOTHETICAL 91.4 KD P	HYPOTHETICAL ABC TRANS	HEAT SHOCK FACTOR PROT	HEAT SHOCK FACTOR PROT	PROTEIN C17/B23.	KPSF PROTEIN.	FERROCHELATASE (EC 4.9	HYPOTHETICAL 33.2 KD P	APOLIPOPROTEIN A-I PRE	PHOSPHOGLYCERATE MUTAS	PROBABLE NA(+)/H(+) AN	PROBABLE STRUCTURAL PR
4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	1.69e+01	1.69e+01

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O'RICKDAN J.L.H., FOITS J.T. JR.; (IN) CALCIUM REQULATING HORMONES, TALMADGE R.V., OMEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975).	ALL H.D., J	BIOCHEMISTRY 17:5723-5729(1978).	Z.	SEQUENCE OF 61-83 AND 84-115.	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).	R.T., JACOBS J.W., KEUTM	111656.	SECUTENCE OF 32-68.	249:155-157(1974).	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;	SEQUENCE OF 26-37.		SCI. U.S.A. 80:2127-2131(1983).	VASICEK T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J., HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;	83169834.	SEQUENCE FROM N.A.	MALE: NORD: COL: C.C.S.	PROC NAME, ACAD SCT U.S.A. 78-7366-7366(1981)	NE; 82150870.	SEQUENCE FROM N.A.	EUTHERIA; PRIMATES.	RYOTA; METAZOA;	HOMO SAPIENS (HUMAN).	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).	(REL. 35, LAST ANNOTATION UPDAY	05,	(REL.	PTHY_HUMAN STANDARD; PRT; 115 AA.	OLT 1

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Query Match
Best Local S
Matches 1
                                                                                                                                                                        HYPOPARATHYROIDISM (FIH).

EMBL; J00301; G190704; -.

EMBL; V00597; G37144; -.

EMBL; V00597; G37144; -.

EMBL; A29146; E186700; -.

PIR; A01536; PPHU

PIR; A19339; A19339.

PDB; 11PH; 10-OUL-95.

PDB; 11PH; 10-OUL-95.

PDB; 12WA; 12-MAR-97.

PDB; 12WC; 16-JUN-97.

PDB; 12WC; 16-JUN-97.

PDB; 12WC; 16-JUN-97.
                                             CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNTHESIS OF 32-65.

MEDLINE; 73227467.

MEDLINE; 73227467.

ANDREATTA R.H., HARTMANN A., JOEHL RINIKER B., RITTEL W., SIEBER P.; HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS. MEDLINE; 7
                                                                                                                                                                                                                                                                                                                                                     ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A., KRONENBERG H.M.;
J. CLIN. INVEST. 86:1084-1087(1990).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SIBONE AND PREVENTING THEIR RENAL EXCRETION.
-!- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95318084.
MARX U.C., AUSTERMANN
STICHT H., WALTER S.,
ROESCH P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF MEDLINE; 93345518.
BARDEN J.A., CUTHBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOCHEMISTRY 30:6936-6942(1991).
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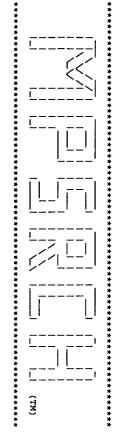
TREGEAR G.W. VAN RIETSCHOTEN J., GREEN E., NIALL H.E KEUTWANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
BIOCHEMISTRY 14:1842-1847(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91299748.
KLAUS W., DIECKMANN T.,
                                                                               VARIANT
                                                                                                                                          PROSITE
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h 100.0%;
Similarity 100.0%;
10; Conservative
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                                                                                                                                          PS00335;
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115
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HEM. 215:315-321(1993).
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                                                                                                                             ; PARATHYROID; 1.
DISEASE MUTATION;
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SCHMID F.-X.,
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Score 73; DB 1; I
Pred. No. 1.53e-06;
0; Mismatches (
                                          PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INE PROCESSING OF THE PRECURSOR)
N -> D (IN REF. 5).
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FORSSMANN W.-G.,
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                        EMBL; J00023; G1636
EMBL; J00024; G1636
EMBL; J00024; E1824
EMBL; J00024; E1825
EMBL; K01938; G1636
EMBL; M25082; G1636
EMBL; M25082; G1636
                                                                                                                                                                   SEQUENCE OF 32-115.
MEDLINE; 71063634.
BREWER H.B. JR., RON
PROC. NATL. ACAD. SC
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21-JUL-1986
01-NOV-1997
                                                                             PROC. NATL. A....
-1- FUNCTION: PTH ELEVATES CALL
BONE AND PREVENTING THEIR RENAL
""ANIAG: G85; -.
        PIR; A01
PIR; A24
PROSITE;
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                                                                                                                                                                                                                       MEDLINE; 71076162.
NIALL H.D., KEUTMANN H.T.,
AURBACH G.D., POTTS J.T. J
                                                                                                                                                                                                                                                                             SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
COHN D.V.;
                                                                                                                                                                                                                                                                                                               GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 80056617.
KRONENBERG H.M., MCDEVITT
POTTS J.T. JR., RICH A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                      POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D. DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.; PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING
                                                                                                                                                                                                                                                                                                                                MEDLINE; 842
WEAVER C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                            PROC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARATHYROID
PTH.
                                                                                                                                                   SYNTHESIS OF 32-65.
                                                                                                                                                                                                                HOPPE-SEYLER'S Z. PHYSIOL.
                                                                                                                                                                                                                                                                           COHN D.
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MEDLINE; 84262483.
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                  A24949; A24949
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83105964.
.A., GORDON
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82037785.
 SIGNAL
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G163641;
G163643;
E18249; ALT_SEQ.
E18250; ALT_INIT.
G163647;
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Search completed: Thu Jul 30 10:10:23 1998 Job time : 8 secs.	δλ β	Qu Be	OS THE THE THE THE THE THE THE THE THE THE
	40 HNLGKHLSSM 49 1 HNLGKHLNSM 10	Query Match 94.5%; Best Local Similarity 90.0%; Matches 9; Conservative	SIGNAL PROPEP CHAIN CONFLICT SEQUENCE
		al Similarity 90.0%; conservative	1 26 32 106 115 AA;
		94.58; 90.08; vative	1 25 26 31 32 115 PARATHYROID HORMONE. 32 115 V -> G (IN REF. 4). 115 AA; 12980 MW; 673EA5F2 CRC32;
		; Score 69; DB 1; Length 115; ; Pred. No. 1.99e-05; 1; Mismatches 0; Indels 0; Gaps	
		0;	





MPsrch_pp 9 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:10:41 1998; MasPar time 4.07 Seconds 103.347 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score: >US-08-817-547A-7 (1-10) from US08817547A.pep

Sequence: 1 HNLGKHLNSM 10

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.281; Variance 24.816; scale 0.898

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 3 3 4 4 5 5 6 6 7 7 7 7 11 11 11 11 11 11 11 11 11 11 1	Result
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110 110 100 100 110 110 111 111 111 111	BB
Q63473 Q63778 Q63778 Q63289 P97692 O32112 Q32112 Q62730 Q36379 Q3	ID
PARATHYROID HORMONE (F HYPOTHETICAL 43.7 KD P L1 RETROPOSON, ORF2 MR L1 RETROPOSON ORF HYPOTHETICAL 48.5 KD P TRANSCRIPTIONAL REGULA 17-BETA HYDROXYSTEROID ATP SYNTHASE A CHAIN (PLAKOGLOBIN (FRAGMENT) TWO-COMPONENT SENSOR K PROSAPOSIN. CHROMOSOME XV READING PLAKOGLOBIN. PLYPOTHETICAL 179.5 KD COMPLETE GENOME (FRAGM HYPOTHETICAL 52.6 KD P HYPOTHETICAL 52.3 KD P COXII INTRON2 ORF. UDD-GLC:GLYCOPROTEIN G	Description
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RL MOL. CELL. BIOL. 6:411-424(1986).

DR EMBL; M13100; G604811; .

KW HYPOTREINA.

SO SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;

QUETY MATCH

Best Local Similarity 66:7%; Ered. No. 1.54e+00;

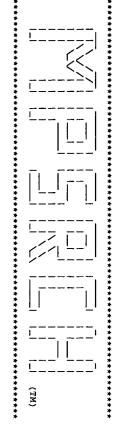
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 74 KLGKHLEHM 82

OY 2 NIJGKHLSHN 10

Search completed: Thu Jul 30 10:11:05 1998

Job time: 24 secs.
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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U Distribution rights by Oxford Molecular Ltd Research Unit. nburgh, U.K.

MPsrch_pp 9 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:14:54 1998; MasPar time 2.63 Seconds 52.587 Million cell updates/sec 2.63 Seconds

Tabular output not generated.

Description: Perfect Score: Title: (1-9) from US08817547A.pep >US-08-817-547A-8

Sequence: 1 NLGKHLNSM

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.754; Variance 55.237; scale 0.285

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15 16 17 18	10 12 14	4384886	No.
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R58263 R58268 R58243 R58229 R58229	W17955 W17947 W20000 R58272 R58219	W17957 W17954 W17968 W17950 W17959 W17969 W17969 W17951 R41557 R41557 R41550	ij
[D-11e5]-hPTH(1-36)-N [Cha8]-hPTH(1-36)-NH2 Propargyl-[Al]-hPTH(1 [Ala30]-hPTH(1-36)-NH [Ala26]-hPTH(1-36)-NH	Human parathyroid hor Human parathyroid hor Cyclised human parath [D-Lys13] -hPTH(1-36)-NH	Human parathyroid hor Human parathyroid hor Human parathyroid hor Human PTH analogue [C Human parathyroid hor Human parathyroid hor [Gln25, 26, 27]hPTH (1- [D-Ala3]hPTH (1-34), Target peptide (PTH(1	Description
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bone fracture
Claim 11; Page -; 33pp; English.
Claim 11; Page -; 33pp; English.
The present sequence is a specific example of a human parathyroid hormone (hPTB) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 is alpha-aminoisobutyric acid (Aib). In this example the Ser residue at position 3 of the wild-type has been substituted by Aib. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in

Dong ZX; WPI; 97-118819/11. New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis

and

Query Match 100.0%; Best Local Similarity 100.0%;

Score Pred. No.

DB 22; 1 3.96e+00;

Length

N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim.

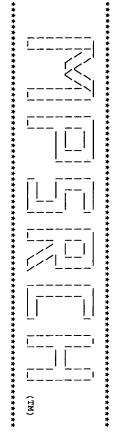
Sequence 34 AA;

20 64 100.0 36 9 R58295 [D-Val35]-hPTH(1-36)- 3.96e+00 21 64 100.0 36 9 R58253 [4-aminobanzota cxidi 3.96e+00 22 64 100.0 38 9 R58252 [Ala0]-hPTH(1-35)-NH2 3.96e+00 23 64 100.0 38 9 R58145 [Ala0]-hPTH(1-35)-NH2 3.96e+00 25 64 100.0 38 9 R58145 [Gly22]-hPTH(1-38)-0H 3.96e+00 26 64 100.0 38 9 R58134 [1e.9]-hPTH(1-38)-0H 3.96e+00 27 64 100.0 38 9 R58134 [1e.9]-hPTH(1-38)-0H 3.96e+00 28 64 100.0 38 9 R58134 [1e.9]-hPTH(1-38)-0H 3.96e+00 29 64 100.0 38 9 R58134 [1e.9]-hPTH(1-38)-0H 3.96e+00 29 64 100.0 47 25 W21946 [4.20]-hPTH(1-38)-0H 3.96e+00 20 64 100.0 47 25 W21946 [4.20]-hPTH(1-38)-3.96e+00 21 64 100.0 84 4 R21180 Human parathyroid hor 3.96e+00 22 64 100.0 84 4 R21180 Human parathyroid hor 3.96e+00 23 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 24 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 25 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 26 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 27 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 28 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 29 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 20 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 21 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 22 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 23 64 100.0 84 4 R21194 Human parathyroid hor 3.96e+00 24 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 25 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 26 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 27 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 28 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 29 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 20 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 21 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 22 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 23 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 24 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 25 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 26 64 100.0 84 4 R21195 Human parathyroid hor 3.96e+00 27 64 100.0 84 4 R	RESULT ID WW ACCOUNT OF THE STATE OF THE STA	00000000000000000000000000000000000000
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II-1997 (first entry) III-1997 (first entry) IIII-1997 (IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	corresponds to the known hPTH 1-34 fragment with the modifica as stated in the claim. Sequence 34 AA;	និនិនិន
W17957; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3 Osteoporosis; agonist; PTH; human; anti- bone fracture. Homo sapiens. Synthetic. Key Homo sapiens. Synthetic. Location/Qualifiers modified_site 34 /label= Aib modified_site 34 //abel= Aib modified_site 34 //ote= "In amide form" W09702834-A1. 30-JAN-1997; US-001105. 06-SEP-1995; US-001105. 06-SEP-1995; US-003305. 29-MAR-1996; US-626186. (BIOM-) BIOMEASURE INC. 29-MAR-1996; US-626186. (BIOM-) BIOMEASURE INC. 29-MAR-1997: H819/11. New variants of human parathyroid hormon stimulate bone growth and are used for the bone fracture Claim 11; Page -; 33pp; English. The present sequence is a specific examp hormone (hPTH) analogue from fragment 1. of the amino acid residues at positions is alpha-aminoisobutyric acid (Aib). In at position 3 of the wild-type has been analogues stimulate bone growth and so a medicine for treatment of osteoporosis a	py (bisphos	888
W1/95/ standard; peptide; 34 AA. W17957; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3 Osteoporosis; agonist; PTH; human; anti- bone fracture. Homo sapiens. Synthetic. Key Homo sapiens. Synthetic. Location/Qualifiers Homo sapiens. Synthetic. Location/Qualifiers Mography (1202) Modified_site 34 modified_site 36 modified_site 34 modifiers Mography (11292) 13-JUL-1995; US-003105 06-SEP-1995; US-003105 06-SEP-1	യയ	នន
W1/95/ Standard; peptide; 34 AA. W17957; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3 Osteoporosis; agonist; PTH; human; anti- bone fracture. Homo sapiens. Synthetic. Key Homo sapiens. Synthetic. Location/Qualifiers modified_site 34 /label= Aib modified_site 34 /note= "In amide form" W09702834-A1. 30-JAN-1997; US-001105. 06-SEP-1995; US-001105. 06-SEP-1995; US-003305. 29-MAR-1996; US-626186. (BIOM-) BIOMEASURE INC. Dong ZX; WPI; 97-118819/11. New variants of human parathyroid hormon stimulate bone growth and are used for t bone fracture Claim 11; Page -; 33pp; English. The present sequence is a specific examp hormone (hPTH) analogue from fragment 1- of the amino acid residues at positions is alpha-aminoisobutyric acid (Abb). In	position 3 of the wild-type has been	ဂ္ဂ
W1/95/ Standard; peptide; 34 AA. W17957; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3]hi Osteoporosis; agonist; PTH; human; anti-res bone fracture. Homo sapiens. Synthetic. Key Homo sapiens. Synthetic. Location/Qualifiers modified_site 3/ Jabel= Aib modified_site 3/ MO9702834-A1. 30-JAN-1997. W09702834-A1. 30-JAN-1995; US-001105. 06-SEP-1995; US-001105. 06-SEP-1995; US-003305. 29-MAR-1996; US-023305. 29-MAR-1996; US-023186. (BIOM-) BIOMEASURE INC. Dong ZX; WPI; 97-118819/11. New variants of human parathyroid hormone : stimulate bone growth and are used for tres bone fracture Claim 11; Page -; 33pp; English. The present sequence is a specific example hormone (hPTH) analogue from fragment 1-34 of the amino acid residues at positions 3	alpha-aminoisobutyric acid (Aib). In	នួន
W1957; standard; peptide; 34 AA. W1957; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Alb3]hPTH(1-34)N Osteoporosis; agonist; PTH; human; anti-resorptive t bone fracture. Homo sapiens. Synthetic. Key Homo sapiens. Synthetic. Key Homo sapiens. Synthetic. Key Homo sapiens. New Homo sapiens. New Homo sapiens. New Homo sapiens. Note= "In amide form" Nog702834-A1. Nog702834	rmone (hPTH) analogue from fragment 1-34	38
W1957 standard; peptide; 34 AA. W1957; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3]hPTH(1-34)N Osteoporosis; agonist; PTH; human; anti-resorptive t bone fracture. Homo sapiens. Synthetic. Key modified_site	a specific example of a human	8
W1957; standard; peptide; 34 AA. W1757; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3]hPTH(1-34)N Osteoporosis; agonist; PTH; human; anti-resorptive t bone fracture. Homo sapiens. Synthetic. Key modified_site 3 modified_site 34 /label= Aib modified_site 34 W09702834-A1. 30-JAN-1997; 03-JUL-1995; US-001105. 13-JUL-1995; US-003105. 06-SEP-1995; US-003105. 06-SEP-1995; US-06186. (BIOM-) BIOMEASURE INC. Dong ZX; WPI; 97-118819/11. New variants of human parathyroid hormone 1-34 pepti bone fracture	-; 33pp; English.	Sď
W1957; W17957 (first entry) 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3]hPTH(1-34)N Osteoporosis; agonist; PTH; human; anti-resorptive t bone fracture. Homo sapiens. Synthetic. Location/Qualifiers modified_site 3/ /label= Aib modified_site 3/ /note= "In amide form" W09702834-A1. 30-JAN-1997; 03-JUL-1995; US-003105. 06-SEP-1995; US-003105. 06-SEP-1995; US-05186. (BIOM-) BIOMEASURE INC. Dong ZX; WPI; 97-118819/11. New variants of human parathyroid hormone 1-34 pepti stimulate bone growth and are used for treatment of	•	ΡŢ
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W1957 standard; peptide; 34 AA. W17957; 29-JUL-1997 (first entry) Human parathyroid hormone analogue [Aib3]hPTH(1-34) Osteoporosis; agonist; PTH; human; anti-resorptive bone fracture. Homo sapiens. Synthetic. Location/Qualifiers modified_site 3 modified_site 34 w09702834-A1. 30-JAN-1997.	U1129	Ä
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PF 13-JUI-1996; U11292.
PR 13-JUI-1995; US-001105.
PR 06-SEP-1995; US-023305.
PR 29-MAR-1996; US-626186.
PA (BIOM-) BIOMEASURE INC.
DR WPI; 97-118819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which PI Dong ZX;
DR WPI; 97-118819/11.
PT New variants of human parathyroid hormone is a specific example of a human parathyroid CC charmone (hPTH) analogue from fragment 1-34 in which at least one PS Claim 11; Page -; 33pp; English.
CC The present sequence is a specific example of a human parathyroid CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 (CC is alpha-aminoisobutyric acid (Aib). In this example the Glu residue CC analogues stimulate bone growth and so are useful in human or veterinary CC conjunction with anti-resorptive therapy (bisphosphonates and CC unicitonin).
CC Corresponds to the known hPTH 1-34 fragment with the modification. It cas stated in the claim.
Sequence 34 AA;
                                                                                                                                                                          RESULT
ID W1
AC W1
DT 29
DE HU
KW OS
KW OS
SW HO
OS SHO
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dest Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43-JUL-1997 (first entry)
Human parathyroid hormone analogue [Aib19]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.
Synthe*ia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W17954 standard; peptide; 34
W17954;
29-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                        10 nlgkhlnsm 18
                                                            μ
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                                                       NLGKHLNSM 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "In amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label- Aib
                                                                                                        Score 64; DB 22; Length 34; Pred. No. 3.96e+00; O; Mismatches O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
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                                                                                                                                      Length 34;
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MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:14:18 1998; MasPar time 3.15 Seconds 104.377 Million cell updates/sec

abular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-8 (1-9) from US08817547A.pep 64 1 NLGKHLNSM 9

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.753; Variance 27.858; scale 0.781

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

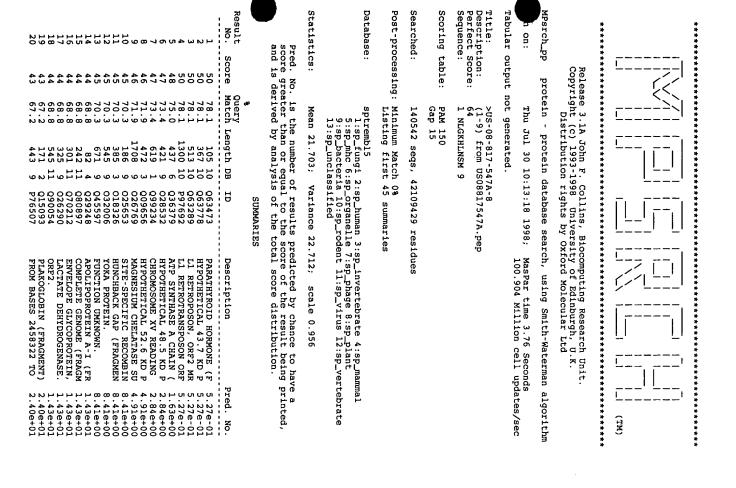
SUMMARIES

1 3 3 4 4 4 4 4 4 6 6 6 7 7 7 7 11 11 11 11 11 11 11 11 11 11 1	sult No.
00000000000000000000000000000000000000	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 93.8 93.8 82.8 82.8 82.8 87.1 78.1 78.1 78.1 78.1 78.1 73.4	Query
34 34 34 35 35 36 37 37 37 37 37 37 37 37 37 37 37 37 37	Length
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	BG
12WA 12WE 12WE 12WF 12WF 12WD 12WD 12WD 12WC 12WC 12WC 12WC 17C4202 PTPG 151851 151851 852014 852014 84863 852014 852014 852311 822310 852311 852311 852311	Ħ
parathyroid hormone (parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 6 parathyroid hormone (parathyroid hormone 6 parathyroid hormone 7 parathyroid hormone 9 probable RNA-directed protein 1 probable membrane 9 hypothetical protein 1 cyclic parathyroid hormone 9 hypothetical protein 1 probable membrane 9 hypothetical protein 1 SEC63 protein complex	Description
2.46e-03 2.46e-03 2.46e-03 2.46e-03 2.46e-03 2.46e-03 2.46e-03 2.66e-02 2.06e-02 2.06e-02 2.06e-02 3.03e+00 3.03e+00 3.03e+00 3.03e+00 1.22e+01 1.91e+01 1.91e+01 1.91e+01	Pred. No.

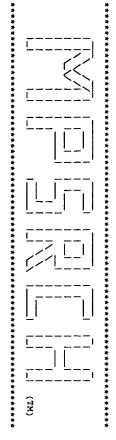
45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
43	43	43	43	44	44	44	44	44	44	44	44	44	45	45	45	45	45	45	46	46	46
67.2	67.2	67.2	67.2	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	70.3		70.3	70.3	70.3	70.3		71.9	
2317	744	738	462	2105	936	585	545	325	298	265	264	231	985	700	671	545	208	186	2068	1708	1490
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156752	A32905	S35093	JC5625	A44059	S64384	G64220	B44054	E69118	C65106	A46018	S31394	JQ0704	S59330	S12053	C69621	E69907	D65041	A64646	A47371	F69189	S32373
c-ros-1 tyrosine kina	plakoglobín, desmosom	plakoglobin – African	Ō	RNA-directed RNA poly	probable membrane pro	ATP-binding protein m	orf2 protein - Junoni	lactate dehydrogenase	3.2 kD	apolipoprotein AI - p	apolipoprotein A-I -		Na+/H+-exchanging pro	protein-tyrosine-phos	fructose-bisphosphata	DNA recombinase homol	hypothetical protein	site-specific recombi	transcription initiat	magnesium chelatase s	DNA-binding protein T
7.12e+01	7.12e+01	7.12e+01	7.12e+01	4.63e+01	4.63e+01	4.63e+01		4.63e+01	4.63e+01	4.63e+01	4.63e+01	4.63e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01		2.99e+01	1.91e+01	1.91e+01	1.91e+01

RESULT 2 1ZWE # TITLE parathyroid ALTERNATE_NAMES HPTH(4-37) PDB_TITLE structure of structure of structures ORGANISM #formal_name REFERENCE A67860 # submitted to # submission submission submission submitted to # submission submissio	Query Match Best Local Simila Matches 9; C Db 10 NLGKHLNSM Qy 1 NLGKHLNSM	o ú	REFERENCE #authors #book COMMENT Resol	ORGANISM #for	RESULT 1 ENTRY TITLE TATERNATE_NAMES PDB_TITLE
12WE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 ROESCH, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nees pDB:12WE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	1 100.0%; Score 64; DB 5; Length 34; Similarity 100.0%; Pred. No. 2.46e-03; 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; SKHLNSM 18	#region helix (right hand alpha)\ #region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629	TN001717 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: NMR loable Determination: NMR loable	#formal_name Homo sapiens #common_name man A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:1ZWA	12WA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures

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COMMENT
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RR	Si	Db Qy	5 B C	FT RAC			US						
EUKARTIS NORVEGICUS (RAT. EUKARVOTA; METAZOA; CHC EUTHERIA; RODENTIA. [1] SEQUENCE FROM N.A. TISSUE-LIVER; MEDLINE; 87064324. D'AMBROSIO E., WAITZKII	01-NOV 01-NOV 01-NOV 01-NOV	tches 31 N 1 N	SEQUENC Query Matc Best Local	SEQUENCE FR SEQUENCE FR TISSUE-THYR SCHMELZER H ADV. GENE T EMBL; M5487 NON TER	PTH. RATTUS EUKARY EUTHER	Q63473 01-NOV 01-NOV 01-JAN PARATH	LT 1 Q63473		54444	3 3 3 7 6	28427	3109876	222
CE FRELIVE	1096 7-1996 7-1996 107-1996	გ — წ	ICE LL Sim	ICE FR :-THYR :ZER H :ENE T M5487	NORV				NNNNN	. w w w u		4444	ω ω ω ω
EGICUMETAZIODENT	(TRE (TRE (TRE 1 43.	Cons ASV 39 : NSM 9	105 AA	FROM N.1 PROID, 1 H.J., (TECHNO) 875; G6(NORVEGICUS (OTA; METAZOA; IA; RODENTIA.	(TRE	P			1 7777	17.7.7	67.2	7777
US (RAT) ZOA; CHO TIA. .A. 24.	RELIMINARY MBLREL. 01 MBLREL. 01 MBLREL. 01 7 KD PROTE	ervat	; 11 78 77 77	AND SROS 21. 2		(TREMBLREL. 01, CR (TREMBLREL. 01, LA (TREMBLREL. 05, LA HORMONE (FRAGMENT)	RELIMINARY		852024	4444	4410101	745 979 1854 2294 2317	44444
2 9.	VARY;	O	146	PARATHYROII S G., MAYEI 1:228-229(1 3;	RAT). CHORDATA;	. 01, . 01, . 05,	NARY;					000000	
	PR CREA LAST LAST	1; M1	MW; 6AC3: Score 5: Pred. N); { H.; [984)		ST	PRT;	ALIGNMENTS	0308 0308 8904 82219 8751	1682	6473 6070 6213 6451	Q15151 Q21962 Q21962 Q63131 Q15265 Q15265 Q63130	1303 2365 2367 7056
VERTEBRATA; TETRAPODA; MAMMALIA; WITNEY F.R., SALEMME A., FURANO A	T; 367 AA. TED) SEQUENCE UPDATE) ANNOTATION UPDATE)	1; Indels 0;	ength 105;	·	VERTEBRATA; TETRAPODA; MAMMALIA;	(PD) SEQUENCE UPDATE) ANNOTATION UPDATE)	105 AA.		REPLICATION PROTEIN A POLYPROTEIN (FRAGMENT) T05A10 1. POLYPROTEIN. PESTIVIRUS POLYPROTEIN				
		Gaps 0;	5						.0000	. 40e+0	.40e+0	2.40e+01 2.40e+01 2.40e+01 2.40e+01 2.40e+01 2.40e+01	. 400e+0



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:12:53 1998; MasPar time 2.12 Seconds 106.569 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-8 (1-9) from US08817547A.pep 64 1 NLGKHLNSM 9

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.743; Variance 23.428; scale 0.971

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

						16						_		_	7				ω	N	L	sult No. Score
٧.	43	43	43	43	44	44	44	44	44	45	45	45	46	46	46	46	50	53	60	60	64	!
67.2	67.2	67.2				68.8	•	•	•	70.3	70.3	70.3	71.9	71.9	71.9	71.9	78.1	82.8	93.8	93.8	100.0	Query Match
	462	313	187	139	2105	936	585	298	265	985	700	208	2068	192	176	152	115	115	115	115	115	Length
. بـ	Н	ш	Н	Ц	<u>بــ</u>	سا	۲	Н	Ь	Н	Н	ب	_	Ь	Ь		⊷	μ,	_	_	-	BB
PLAK_MOUSE	CISY_TETTH	LDH_METJA	ATPD_ODOSI	STBB_PSESM	POLR_ASGVP	YG2K_YEAST	Y187_MYCGE	YHBV_ECOLI	APA1_PIG	NAH_YEAST	PTPE_HUMAN	YFJJ_ECOLI	CCG1_DROME	SC72_YEAST	HMGA_SOYBN	HMGB_SOYBN	PTHY_RAT	PTHY_PIG	PTHY_CANFA	PTHY_BOVIN	PTHY_HUMAN	IJ
JUNCTION PLAKOGLOBIN (CITRATE SYNTHASE, MITO	L-LACTATE DEHYDROGENAS	ATP SYNTHASE DELTA CHA	PLASMID STABILITY PROT	GENOME POLYPROTEIN (CN	HYPOTHETICAL 106.5 KD	HYPOTHETICAL ABC TRANS	HYPOTHETICAL 33.2 KD P	APOLIPOPROTEIN A-I PRE	PROBABLE NA(+)/H(+) AN	PROTEIN-TYROSINE PHOSP	HYPOTHETICAL 24.6 KD P	TRANSCRIPTION INITIATI	TRANSLOCATION PROTEIN	HMG-Y RELATED PROTEIN	HMG-Y RELATED PROTEIN	PARATHYROID HORMONE PR	Description				
2.21e+01	2.21e+01	2.21e+01	2.21e+01	2.21e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	7.96e+00	7.96e+00	7.96e+00	4.71e+00	4.71e+00	4.71e+00	4.71e+00	5.29e-01	9.45e-02	1.35e-03	1.35e-03	1.05e-04	Pred. No.

45	44	43	42	41	40	39	38	37	36	3 5	34	ω	32	31	30	29	28	27	26	25	24
41	4	41	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	43	43
64.1	64.1				65.6		٠						•	•	•						
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KPL1_HUMAN	VA32_VARV	PMGY_MYCTU	TEGU_HSV7J	RRPL_RDV	BIMC_EMENI	IMB3_HUMAN	YSPL_CAEEL	YAN4_SCHPO	HSF1_HUMAN	YD05_YEAST	SMI1_YEAST	HSF1_MOUSE	YBQ6_YEAST	KIPA_BPT7	PFTB_CAEEL	PMGY_MYCLE	SRIA_PHYPO	YYAN_BACSU	SLIB_HUMAN	BICD_DROME	PLAK_HUMAN
SERINE/THREONINE PROTE	PROTEIN A32.	PHOSPHOGLYCERATE MUTAS	LARGE TEGUMENT PROTEIN	RNA-DIRECTED RNA POLYM	KINESIN-LIKE PROTEIN B	IMPORTIN BETA-3 SUBUNI	HYPOTHETICAL 91.0 KD P	ã	HEAT SHOCK FACTOR PROT	HYPOTHETICAL 60.9 KD P	SMI1 PROTEIN (KILLER T	HEAT SHOCK FACTOR PROT	HYPOTHETICAL 57.8 KD P	PROTEIN KINASE (EC 2.7	PROBABLE PROTEIN FARNE	PHOSPHOGLYCERATE MUTAS	SPHERULIN 1A PRECURSOR	HYPOTHETICAL TRANSCRIP	SOMATOLIBERIN PRECURSO	CYTOSKELETON-LIKE BICA	JUNCTION PLAKOGLOBIN (
	5.90e+01	5.90e+01	3.63e+01	3.63e+01	3.63e+01	3.63e+01	3.63e+01	3.63e+01			3.63e+01	2.21e+01	2.21e+01								

(1975). [7]	RI.
J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION	RL
	RĽ
H., POTTS J.T. JR.;	RA
Ξ.	RΑ
SEQUENCE OF 75-100.	R X
BIOCHEMISTRY 17:5723-5729(1978).	RE
	RA
KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,	RA
855.	RX
SEQUENCE OF 61-83 AND 84-115.	RP
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SCI. U.S.A. 71:384-388(1	RĽ
.L.H., AURBACH G.D., POTTS J.T. JR.;	RA
	RA :
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NAMIDE DAGGIAS-1977/1974)	3 5
E; 74174967.	RX
SEQUENCE OF 26-37.	RP
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OTTS J.T. JR., RICH A., KRONENBERG H.N	RA
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SEQUENCE FROM N.A.	RP
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G.N., KRONENBERG H.M.	RA
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[1]	RN
PRIMATES.	88
PYOTA: METAZOA:	3
HOMO SAPIENS (HUMAN).	S S
PARATHIROID HORMONE PRECURSOR (PARATHIRIN) (PTH).	E
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7 (REL. 05,	DŦ
1986 (REL.	D.
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ACTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALT.

LOSEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED DR EMBL; VO0557; 637144; ---
DR EMBL; V00557; 637144; ---
DR EMBL; A01336; FTHU.

PDB; 1174; 115-CCT-97.
PDB; 1274; 12-MAR-97.
DR PDB; 1274; 12-MAR-97.
DR
                                                                                                  DR DR FTT FTT FTT SQ
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Best Local S
Matches
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                                                                                                                                                       CHAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT ARG-18.

VARIANT ARG-18.

WEDLINE; 91009811.

ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

KRONENBERG H.M.;

J. CLIN. INVEST. 86:1084-1087(1990).

J. FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS

OF FAMILIAL ISOLATED
                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                SIGNAL
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MEDLINE; 95318084.
MARX U.C., AUSTERWANN S., BAYER P.,
STICHT H., WALTER S., SCHMID F.-X.,
ROESCH P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 93345518
BARDEN J.A., CUTH
EUR. J. BIOCHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 32-65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 75059220.
TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D., KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS.
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T.
BIOCHEMISTRY 14:1842-1847(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNTHESIS OF 32-65. MEDLINE; 73227467.
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            Similarity 100.0%;
9; Conservative
                                                                                                                                             2; SIGNAL; DISEASE 1 25 26 31 32 115 18 18
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115 AA;
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HEM. 215:315-321(1993).
                                                                                                                                                                                                                      PARATHYROID; 1.
DISEASE MUTATION;
                                                                                         107
12861
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          Score 64; DB 1; I
Pred. No. 1.05e-04;
0; Mismatches 0
                                                                             PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEFFICIENT PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
243E87C7 CRC32;
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                                                                                                                                                                                                                  3D-STRUCTURE.
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Gaps
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RESULT
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EMBL; V000106; G85; ...
EMBL; V000106; G85; ...
EMBL; J00023; G163641; ...
EMBL; J00024; E18249; ALT_SEQ.
EMBL; J00024; E18250; ALT_INIT.
EMBL; K01938; G163647; ...
EMBL; M25082; G163645; ...
EMBL; M25082; G163645; ...
PIR; A01534; PTBO.
PIR; A04949; A24949.
PROSITE; PS00335; PARATHYROID; 1.
HORMONE; SIGNAL.
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BREWER H.B. (
PROC. NATL. )
                                                                                                                                                                                                                                                             PROC.
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NIALL H.D., KEUTMANN H.T.,
AURBACH G.D., POTTS J.T. J.
HOPPE-SEYLER'S Z. PHYSIOL.
                                                                                                                                                                                                                                                                                                                 MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 32-115.
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MEDLINE; 71076162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
COHN D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 84262483.
MEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRONENBERG H.M., MCDEVITT B.E., POTTS J.T. JR., RICH A., PROC. NATL. ACAD. SCI. U.S.A. 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOS TAURUS EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986
21-JUL-1986
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARATHYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTHY_BOVIN P01268;
                                                                                                                                                                                            LINE: 71091588.

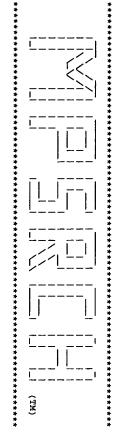
TS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., TOS L.J., DAWSON B.F., HOGAN M.L., AUBACH G.D., C. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE BONE AND PREVENTING THEIR RENAL EXCRETION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41
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u.B. JR., RONAN R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOVINE).
METAZOA; CHORDATA; VERTEBRATA;
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, GORDON D.F., )
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01, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                JR.;
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.S.A. 78:4073-4077(1981).
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Ş 밁 SOFT Query Match 93.8%; Score 60; DB 1; Length 115; Best Local Similarity 88.9%; Pred. No. 1.35e-03; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps SIGNAL PROPEP CHAIN CONFLICT SEQUENCE 1 25 26 31 32 115 PARATHYROID HORMONE. 32 115 V -> G (IN REF. 4). 106 106 V -> G (IN REF. 4). 115 AA; 12980 MW; 673EA5F2 CRC32; ,0

Search completed: Thu Jul 30 10:12:59 1998 Job time: 6 secs.





MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

9: Thu Jul 30 10:17:12 1998; MasPar time 2.69 Seconds 45.680 Million cell updates/sec

Rabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-9 (1-8) from US08817547A.pep 59 1 LGKHLNSM 8

Scoring table: PAM 150 Gap 15

ALIGNMENTS

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.458; Variance 50.932; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11111111111111111111111111111111111111	Result
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Score
110000000000000000000000000000000000000	Query Match
	Length 1
2222 2222 2222 2222 2222 2222 2222 2222 2222	80
W20000 W17949 W17955 W17950 W17950 W17951 R22293 W17951 R41550 R41550 R41550 R98951 R41550 R98951 R41550 R98951 R58263 R58268 R58229 R58229 R58299	ij
Cyclised human parath Human parathyroid hor [Gln25,26,27]hpFH (1-34). Target peptide (PTH(1 Target peptide (PTH(1 Human parathyroid hor [D-11e5]-hpTH(1-36)-NH [Cha8]-hpTH(1-36)-NH [Pro35]-hPTH(1-36)-NH	Description
7.14e+00 7.14e+00	Pred. No.

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11 lgkhlnsm 18

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	24
59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	,
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.1	ř	.14	.1	.1.	1,	. 1 4	Ŀ	.1	ř	7,	ĭ				7.14e+00				. 1.	. 14	.14e+	7.14e+00	.14e+	•	•

% A O	រិធិស្សស្សស្ស	קק אל	X + + + + + + + 0 X + + + + + + + 7	RES DE DE S KW
Query Match 100.0%; Score 59; DB 22; Length 34; Best Local Similarity 100.0%; Pred. No. 7.14e+00; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps	Claim 6; Page -: 23pp; English. W20000 is a cyclised peptide derived from the N-terminal sequence of human parathyroid hormone (PTH). The peptide is able to bind to PTH receptors and stimulate adenylate cyclase activity. Cyclised PTH peptides stimulate bone growth and thus are useful in the treatment of osteoporosis and bone fractures. Optionally they may be administered concurrently with antiresorptive therapy (e.g. bisphosphonate and calicitonin). N.B. sequence not given in the specification, created from known sequence of amino acids 1-34 of human PTH.	19-DEC-1996. 06-JUN-1996; U09674. 07-JUN-1996; U09674. 07-JUN-1995; US-488105. 07-JUN-1995; US-488105. (BETH-) BETH ISRAEL HOSPITAL ASSOC. Chorev M, Rosenblatt M; WPI; 97-051884/05. WPI; 97-051884/05. New cyclic analogues of parathyroid hormone - having disulphide or amide bond between residues 13 and 17 and/or between residues 26 and 30. useful for treating osteoporosis and hone fractures	Homo sapiens. Key misc_difference 26 /note= "joined via amide bond to residue 30" misc_difference 30 /note= "joined via amide bond to residue 26" misc_difference 34 /note= "amidated" W09640193-A1.	RESULT 1 ID W20000 standard; peptide; 34 AA. RC W20000; DE W20000; Cyclised human parathyroid hormone (1-34) amide. RW Parathyroid hormone; PPH; amino terminus; cyclic; analogue; RW adenylate cyclase activity; bone growth; osteoporosis; fracture; RW antiresorptive therapy.

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RESULT AC WILL ACCOUNT ACCOUNT
Search completed: Thu Jul 30 10:17:29 1998 Job time: 17 secs.
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DR WPI; 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which PT stimulate bone growth and are used for treatment of osteoporosis and PT stimulate bone growth and are used for treatment of osteoporosis and PT stimulate bone growth and are used for treatment of osteoporosis and PT stimulate bone growth and are sequence is a specific example of a human parathyroid CC bone and cald residues at positions 7, 11, 23, 24, 27, 28 and 31 cc cyclohaxylalanine (cha). In this example the Trp residue at position 31 of the cc wild-type have been substituted by Cha. The hPTH analogues stimulate CC wild-type have been substituted by Cha. The hPTH analogues stimulate treatment of osteoporosis and bone fracture, optionally in conjunction CC with anti-resorptive therapy (bisphosphonates and calcitonin).

CC N.B. The present sequence does not appear in the specification. It as stated in the claim.

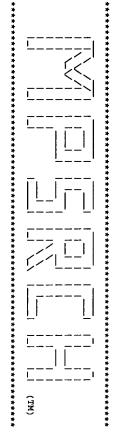
Sequence 34 AA;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative
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30-JAN-1997.
30-JUL-1996; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W17949 standard; peptide; 34 AA.
W17949;
W17949;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha24,28,31]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.
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/note- "Cha"
31
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/note= "In amide form"
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/note= "Cyclohexylalanine (Cha)"
28
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/note= "Cha"
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                                                                                                                                                                                                                                     Score 59; DB 22; Le
Pred. No. 7.14e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 Length 34;
                                                                                                                                                                                                                                        Indels
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FT SIGNAL 1 25
FT PROPEP 26 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;
Query Match 92.2%; Score 47; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 1.19e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 43 GKHLSSM 49
| | | | | | | | |
Oy 1 GKHLNSM 7

Search completed: Thu Jul 30 10:17:55 1998

Job time: 8 secs.
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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:15:51 1998; MasPar time 3.14 Seconds 93.097 Million cell updates/sec

Pabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-9 (1-8) from US08817547A.pep 59

1 LGKHLNSM 8

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 21.301; Variance 26.286; scale 0.810

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

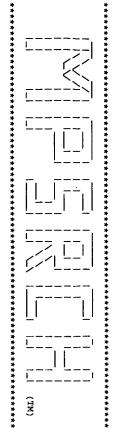
SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	ъ	4	ω	N	ب	Sult No.
45	45	45	45	45	46	46	46	47	47	48	49	55	55	55	59	59	59	59	59	59	59	59	Score
6	რ	76.3		76.3	78.0		8	79.7	9			ω.	ω.	93.2			٠	100.0	100.0		100.0	100.0	Query Match
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S32373	S59330	E69907	A05091	I51851	A53835	S22310	S22311	S48853	S52014	PTPG	S21976	PTBO	JC4202	1ZWC	PTHU	1HPH	1ZWB	1 ZWD	1ZWF	1ZWG	1ZWE	12WA	Ħ
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RESULT 2 ENTRY INTER PARATE NAMES HPTH(4-37) PDB_TITLE ORGANISM REFERENCE # structure # formal_name Homo sapiens #common_name man Resch. P: Marx, U.C. # submission submitted to the Brookhaven Protein Data Bank, June 1996 REFERENCE # cross-references PDB:1ZWE REFERENCE # authors # submitted to the Brookhaven Protein Data Bank, June 1996 REFERENCE # TN001721 # authors Marx, U.C. # submission submitted to the Brookhaven Protein Data Bank, June 1996 REFERENCE TN001701 # authors In Strukturen Verschiedener Parathormonfragmente in Loese # submitted to the Brookhaven Protein Data Bank, June 1996 REFERENCE TN001701 # authors In Strukturen Verschiedener Parathormonfragmente in Loese # pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	Query Match 100.0%; Score 59; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 1.45e-02; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps Db 11 LGKHLNSM 18	COMMENT Determination: NKR KEYWORDS hormone FEATURE 6-9 #region helix (right hand alpha)\ 19-30 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4118 #checksum 5629	CE TROO1717 CE MATX, U.C. hors in Strukturen Verschiedener Parathormonfragmente in k in Strukturen Verschiedener Parathormonfragmente in k pp.0, Bayreuth : University of Bayreuth (Thesis), Resolution: not applicable		RESULT 1 IZWA #type complete TITLE parathyroid hormone (residues 1-34) - human ALTERNATE_NAMES HPTH(1-34) PDB_TITLE structures Structures
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Search completed: Thu Jul 30 10:16:15 Job time : 24 secs.	COMMENT Resolution: not appl COMMENT Determination: NMR REYWORDS hormone FEATURE 15-25 SUMMARY #region h SUMMARY #length 34 #m Ouery Match Best Local Similarity 100.0%; Matches 8; Conservative Db 8 LGKHLNSM 15 Oy 1 LGKHLNSM 8
Jul 30 10:16:15 1998	Resolution: not applicable Determination: NMR hormone #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508 ch 100.0%; Score 59; DB 5; Length 34; 1 Similarity 100.0%; Pred. No. 1.45e-02; 8; Conservative 0; Mismatches 0; Indels 0; GKHLNSM 15
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MPsrch_pp on : protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:15:27 1998; MasPar time 2.12 Seconds 94.808 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-9 (1-8) from US08817547A.pep 59

Sequence: 1 LGKHLNSM 8

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.280; Variance 22.155; scale 1.006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SEQUENCE
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--- FUNCTION: PTH ELEVARES CALCIUM LEVEL BY DISSOLVING THE SALTS BONE AND PREVENTING THEIR RENAL EXCRETION.

---- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED HYPOPARATHYROIDISM (FIH).

EMBL; J00301; G190704; ---
EMBL; V00597; G37144; ---
EMBL; A29146; E186700; ---
EMBL; A29146; E186700; ---
EMBL; A19339; A19339.

PIR; A19339; A19339.

FIR; A19339; A19339.

FIR; A19339; A19339.

FIR; A19339; A19339.
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ARNOLD A., HORST S.A.,
KRONENBERG H.M.;
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STICHT H., WALTER S., SCHMID F.-X.,
ROESCH P.
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BARDEN J.A., CUTHBERTSON R.M.;
BUR. J. BIOCHEM. 215:315-321(1993).
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MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
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TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS

KEUTMANN G.Z. PHYSIOL. CHEM. 355:415-421(1974).
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                     Local
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MEDLINE: 73227467.
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MEDLINE; 75146516.
MEDLINE; 75146516.
MEGUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
BIOCHEMISTRY 14:1842-1847(1975).
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1ZWB;
1ZWC;
1ZWD;
1ZWE;
       h 100.0%;
Similarity 100.0%;
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115
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N -> D (IN REF. 5).
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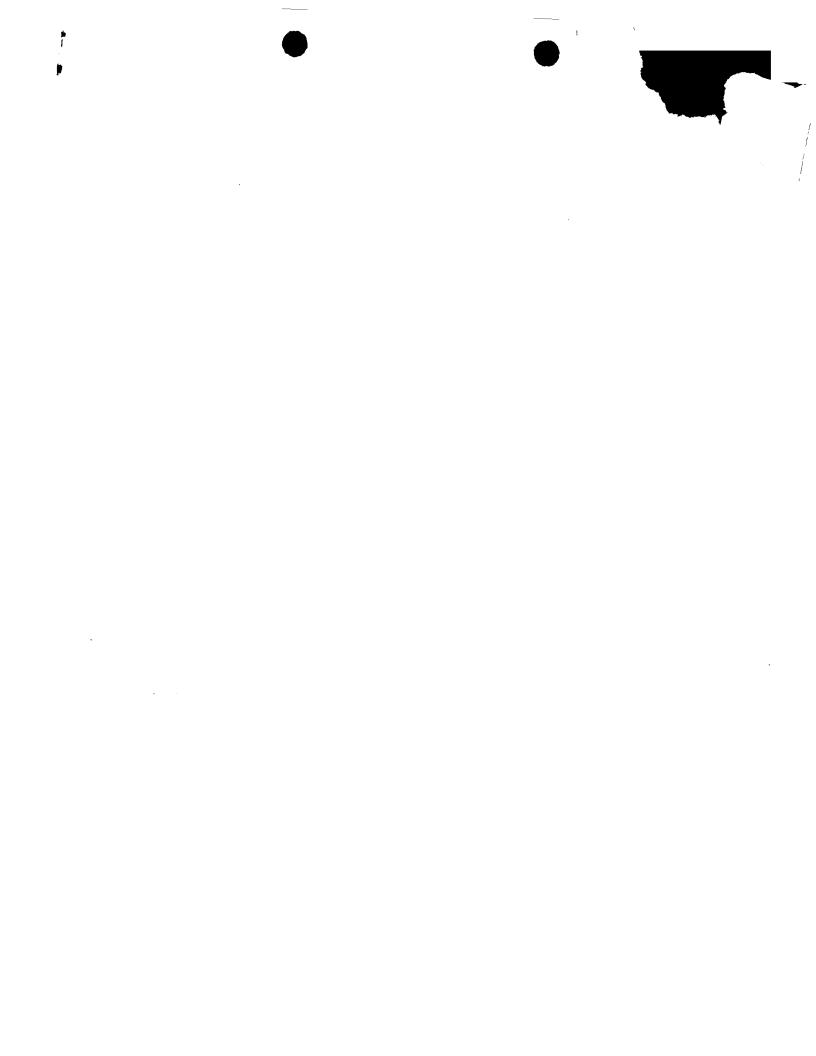
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BREWER H.B.
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NIALL H.D., KEUTMANN H.T., SI
AURBACH G.D., POTTS J.T. JR.
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MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
COHN D.V.;
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MEDLINE; 71076162.
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WEAVER C.A., GORDON D.
MOL. CELL. ENDOCRINOL.
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PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
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3.A. 78:4073-4077(1981).
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                                                                                                                                                                                                                                                                       NIALL H.D.,
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                                                                                                                                                                                                               THE SALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTTS
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                                                                                                                                                                                                                                                                       SAUER
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F
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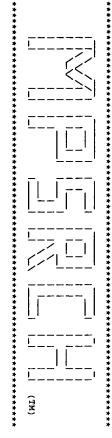
PIR; A01534; PTBO.
PIR; A24949; A24949.
PROSITE; PS00335; PAI

SIGNAL

PARATHYROID;

Sear Job	Оу	Ma Be	SPFFFF
Search completed: Thu Jul 30 Job time : 7 secs.	42 LGKHI 1 LGKHI	Query Match Best Local Si Matches 7	SIGNAL PROPEP CHAIN CONFLICT SEQUENCE
d: Thu Jucs.	LGKHLSSM 49	y Match 93.2%; Local Similarity 87.5%; hes 7; Conservative	1 26 32 106 115 AA;
		93.2%; 87.5%; rvative	25 31 115 106 V
10:15:34 1998		Score 55; DB 1; Length 115; Pred. No. 1.20e-02; 1; Mismatches 0; Indels	PARATHYROID HORMONE. V -> G (IN REF. 4). W; 673EA5F2 CRC32;
		yth 115; Indels	
		0;	
		Gaps	
		0;	





MPsrch_pp 92: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:16:32 1998; MasPar time 3.68 Seconds 91.451 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: (1-8) from US08817547A.pep 59 >US-08-817-547A-9

Sequence: 1 LGKHLNSM 8

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mbc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent I1:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.247; Variance 21.504; scale 0.988

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	Ħ	Description	Pred. No.
1	49	83.1	367	5	Q63778	HYPOTHETICAL 43.7 KD P	4.51e-01
2	49	83.1	513	10	Q63289	L1 RETROPOSON, ORF2 MR	4.51e-01
ω	49	83.1	1300	10	P97692	L1 RETROTRANSPOSON ORF	4.51e-01
4	47	79.7	437	σ	Q36379	ATP SYNTHASE A CHAIN (1.45e+00
տ	46	78.0	472	ω	Q09656	HYPOTHETICAL 52.6 KD P	2.58e+00
σ	45	76.3	105	10	Q63473	PARATHYROID HORMONE (F	4.53e+00
7	45	76.3	545	φ	032006	YOKA PROTEIN.	4.53e+00
8	44	74.6	82	4	Q29248	APOLIPOPROTEIN A-I (FR	7.90e+00
9	44	74.6	242	11	Q80897	COMPLETE GENOME (FRAGM	7.90e+00
10	44	74.6	301	11	Q70212	ENVELOPE GLYCOPROTEIN,	7.90e+00
11	44	74.6	325	9	026290	LACTATE DEHYDROGENASE.	7.90e+00
12	44	74.6	619	_	Q99234	CHROMOSOME XV READING	7.90e+00
13	44	74.6	671	9	Q45597	FUNCTION UMKNOWN.	7.90e+00
14	43	72.9	171	N	Q15093	PLAKOGLOBIN (FRAGMENT)	1.36e+01
15	43	72.9	554	w	Q23651	ZK863.3.	1.36e+01
16	43	72.9	719	ω	017828	C08F8.2.	1.36e+01
17	43	72.9	745	N	Q15151	PLAKOGLOBIN.	1.36e+01
18	43	72.9	745	10	P70565	PLAKOGLOBIN.	1.36e+01
19	43	72.9	1708	9	026769	MAGNESIUM CHELATASE SU	1.36e+01
20	42	71.2	107	10	Q60549	GROWTH HORMONE-RELEASI	2.33e+01

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
41	41	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
	69.5															71.2								71.2
545 11	164 12					2466 2		2460 10					979 3			646 10								226 11
. 090054	2 Q92037							_	_	215265			021962	_	_	063779		Q41770						P89049
ORF2.	NITRIC-OXIDE SYNTHASE	PESTIVIRUS POLYPROTEIN	PROTEIN TYROSINE PHOSP	PROTEIN TYROSINE PHOSP	BA14 TYROSINE PHOSPHAT	PROTEIN-TYROSINE-PHOSP	PROTEIN TYROSINE PHOSP	PROTEIN TYROSINE PHOSP	PROTEIN-TYROSINE PHOSP	PROTEIN TYROSINE PHOSP	POLYPROTEIN (FRAGMENT)	STRUCTURAL POLYPROTEIN	SIMILAR TO GLYCINE DEH	T32G6.14 PROTEIN.	DNA MISMATCH REPAIR PR	HYPOTHETICAL 76.2 KD P	PROSAPOSIN.	ALPHA-AMYLASE.	HYPOTHETICAL 48.5 KD P	IRON-SULFUR CLUSTER BI	BACILLUS SP. MANNAN EN	REPLICATION PROTEIN A	HOMOLOGUE TO PROTEIN E	E0/E2 (FRAGMENT).
3.94e+01			2.33e+01	2.33e+01		2.33e+01	2.33e+01		•	2.33e+01	2.33e+01	2.33e+01	2.33e+01			2.33e+01	2.33e+01	2.33e+01	2.33e+01	2.33e+01	2.33e+01	2.33e+01	2.33e+01	2.33e+01

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Best Local Similarity 75.0%;
Matches 6; Conservative
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Q63778;
Q63778;
Q63778;
Q1-NOV-1996 (TREMBLREL 01, CRE
Q1-NOV-1996 (TREMBLREL 01, LAS
Q1-NOV-1996 (TREMBLREL 01, CRE
SEQUENCE FROM N.A. TISSUE-LIVER; MEDLINE; 92375092. ILVES H., KAHRE O., 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER:
MEDLINE: 87064324.
D'AMBROSIO E., WAITZKIN S.D., WITNEY F.R.,
MOL. CELL. BIOL. 6:411-424(1986).
EMBL; M13100; G804811; -.
EMBL; M13100; G804811; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                 LT 2
Q63289
PRELIMINARY; PRT; 513 AA.
Q63289;
O1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMBLEL. 01, LAST ANNOTATION UPDATE)
L1 RETROPOSON, ORF2 MRNA (PARTIAL) (FRAGMENT).
RATTUS NORVEGICUS (RAT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 LGKHLEHM 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LGKHLNSM 8
                                                                                                                                                                RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
      SPEEK M.;
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01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 10
Pred. No. 4.51e-
1; Mismatches
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No. 4.51e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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DR EMBL: MAN TER 5129; G56522; ...
FI NON TER 5129; G56522; ...
50 SEQUENCE 513 AA; 60414 MW; 3EB70B62 CRC32;

QUARTY MAtch 83.1%; Score 49; DB 10; Length 513;

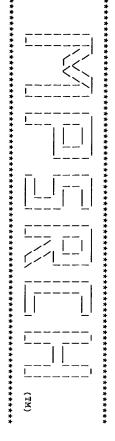
Best Local Similarity 75.0%; Pred. No. 45.1e-01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 423 LGKHLEHM 430

Gy 1 LGKHLNSN 8

Search completed: Thu Jul 30 10:16:53 1998

Search completed: Thu Jul 30 10:16:53 1998
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MPsrch_pp 9 9 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:20:02 1998; MasPar time 2.67 Seconds 40.289 Million cell upda

updates/sec

Title: abular output not generated. >US-08-817-547A-10

Description: Perfect Score: Sequence: (1-7) from US08817547A.pep 1 GKHLNSM 7

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.516; Variance 40.392; scale 0.359

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	œ	7	თ	ഗ	4	ω	N	ч	esult No.
51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	٠	100.0	100.0	•	100.0	100.0	•	٠	100.0	100.0	Query Match Le
36	36	36	36	36	36	36							34					27	Length 1
9	9	9	ø	ဖ	9	9	22	22	22	9	22	22	7	22	22	22	22	ω	BB
R58026	822	R58268	R58267	R58170	R58177	R58243	W17947	W17944	W17943	R98951	տ	ā	R34355	W17950	W17955	W17954	W17939	P82185	ID
N-alpha-methyl[Ala1]	[Ala30]-hPTH(1-36)-NH	[Cha8]-hPTH(1-36)-NH2	[Phe8]-hPTH(1-36)-NH2	[Nva1]-hPTH(1-36)-NH2	[Morpholine-2-carboxy	Propargyl-[A1]-hPTH(1	Human parathyroid hor	Human parathyroid hor	parathyroi	Target peptide (PTH(1	Human parathyroid hor	Human PTH analogue [C	Human parathyroid hor	Human PTH analogue [C	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Sequence of parathyro	Description
1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	Pred. No.

51 100.0 37 9 R88244 [Ala0]-hprH(1-36)-NH2 51 100.0 38 9 R58145 [Leu21]-hprH(1-38)-OH 51 100.0 38 9 R58145 [Gly22]-hprH(1-38)-OH 51 100.0 38 9 R58075 [Ser33]-hprH(1-38)-OH 51 100.0 38 9 R58075 [Gly33]-hprH(1-38)-OH 51 100.0 38 9 R58078 [Gly33]-hprH(1-38)-OH 51 100.0 38 9 R58078 [Met19]-hprH(1-38)-OH 51 100.0 44 26 P30015 Human parathyroid hor 51 100.0 84 4 R21180 Human parathyroid hor 51 100.0 84 4 R21120 Human parathyroid hor 51 100.0 84 4 R21120 Human parathyroid hor 51 100.0 84 4 R23223 Human parathyroid hor 51 100.0 84 4 R23223 Human parathyroid hor 51 100.0 84 4 R23226 Human parathyroid hor 51 100.0 84 4 R23227 Human parathyroid hor 51 100.0 84 4 R23227 Human parathyroid hor 51 100.0 84 4 R23227 Human parathyroid hor 51 100.0 84 4 R23228 Human parathyroid hor 51 100.0 84 4 R23229 Human parathyroid hor 51 100.0 84 4 R23229 Human parathyroid hor 51 100.0 84 4 R23237 Human parathyroid hor 51 100.0 84 4 R23139 Human parathyroid hor
37 9 R58244 [AlaO]-hPTH(1-36) 38 9 R58145 [Gly22]-hPTH(1-38) 38 9 R58145 [Gly22]-hPTH(1-38) 38 9 R58075 [Gly33]-hPTH(1-38) 38 9 R58076 [Gly33]-hPTH(1-38) 38 9 R58078 [Gly33]-hPTH(1-38) 38 19 R58078 [Met19]-hPTH(1-38) 44 26 P30015 Human parathyroid 47 25 W21946 Fusion protien con 47 27 W25687 Human parathyroid 48 4 R21180 Human parathyroid 48 4 R21181 Human parathyroid 48 4 R21220 Human parathyroid 48 4 R23223 Human parathyroid 48 4 R23223 Human parathyroid 48 4 R23226 Human parathyroid 48 4 R23227 Human parathyroid 48 4 R23227 Human parathyroid 48 4 R23229 Human parathyroid 48 4 R23237 Human parathyroid 58 4 R23237 Human parathyroid 58 4 R23237 Human parathyroid 59 R5814
9 R58244 [Ala0]-hpTH(1-36)- 9 R58145 [G1y22]-hpTH(1-38) 9 R58145 [G1y22]-hpTH(1-38) 9 R58075 [Ser33]-hpTH(1-38) 9 R58075 [G1y33]-hpTH(1-38) 9 R58078 [G1y33]-hpTH(1-38) 9 R58128 [Met19]-hpTH(1-38) 19 R58128 [Met19]-hpTH(1-38) 26 P30015 Human parathyroid 4 R21180 Human parathyroid 4 R21181 Human parathyroid 4 R21120 Human parathyroid 4 R23223 Human parathyroid 4 R23223 Human parathyroid 4 R21227 Human parathyroid 4 R23237 Human parathyroid 5 R23237 Human parathyroid 6 R23237 Human parathyroid 7 R346694 Sequence of varian
9 R58244 [Ala0]-hpTH(1-36) 9 R58145 [GLeu21]-hpTH(1-38) 9 R58075 [G273]-hpTH(1-38) 9 R58076 [G1y3]-hpTH(1-38) 9 R58076 [G1y3]-hpTH(1-38) 9 R58078 [G1y3]-hpTH(1-38) 9 R58078 [Met19]-hpTH(1-38) 9 R58078 [Met19]-hpTH(1-38) 9 R58128 [Met19]-hpTH(1-38) 9 R58128 [Met19]-hpTH(1-38) 9 R58128 [Met19]-hpTH(1-38) 9 R58128 [Met19]-hpTH(1-38) 1 R2180 Human parathyroid 4 R21180 Human parathyroid 4 R21181 Human parathyroid 4 R2323 Human parathyroid 4 R21227 Human parathyroid 5 W29420 Human parathyroid 6 R23243 Human parathyroid 7 R34460 Human parathyroid 8 R21226 Human parathyroid 8 R21227 Human parathyroid 8 R23237 Human parathyroid 8 R21218 Human parathyroid 8 R21219 Human parathyroid 8 R21219 Human parathyroid 8 R21219 Human parathyroid 8 R21219 Human parathyroid 8 R49694 Sequence of varian
[Ala0]-hprH(1-36) [Lau2]-hprH(1-36) [Gly22]-hprH(1-38) [Gly22]-hprH(1-38) [Ser33]-hprH(1-38) [Gly33]-hprH(1-38) [Met19]-hprH(1-38) Human parathyroid Fusion protien com Human parathyroid

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RESULT
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AC WI
DT 2:
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                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                     Parathyroid hormone peptide analogues - used for treating osteoporosis, hypercalcaemia, hyperparathyroidism and hormone dependent tumours, and in vitro for bio:assays Claim 3; column 8; 5pp; English.

The PTH analogues of the invention are used for inhibiting the naturally-occurring hormone in vivo and in vitro. They have high binding affinity for their resp. cell surface receptors while not stimulating prodn. of second messenger molecules. They may be used in vitro in a bioassay for PTH and in vivo for therapy and diagnosis. They are prepd. in dosage forms for oral, parenteral, rectal, intranasal or topical admin.
W17939 standard; peptide; 34 AA.
W17939;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-1988.
26-MAY-1987; US-054359.
26-MAY-1987; US-054359.
(MERI ) MERCK & CO INC.
ROSenblatt M, Caporale LH, Nutt RF, Levy JJ, Chorev M; WPI; 88-278169/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1992 (first entry)
Sequence of parathyroid hormone (PTH) analogue [L-Phe23]hPTH(7-34)NH2.
Parathyroid hormone analogue; osteoporosis therapy; hypercalcaemia;
hyperparathyroidism; hormone dependent tumour; bloassay; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P82185 standard; Protein; 27 AA. P82185; 06-MAR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
US4771124-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment.
                                                                                                                     1 GKHLNSM 7
                                                                                                                                             6 gkhlnsm 12
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                     Score 51; DB 3;
Pred. No. 1.10e+01
                                                                                                                                                                                       0,:
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                     Length
                                                                                                                                                                                       0,
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                       27;
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                                                                                                                                                                                      Gaps
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밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone fracture

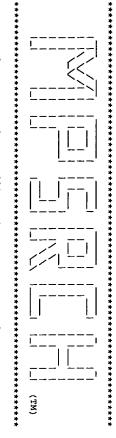
Claim 5; Page -; 33pp; English.

Claim 5; Page -; 33pp; English.

The present sequence is a specific example of a human parathyroid formone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 crossition and the Leu at positions 11 in the wild-type have been crossition 7 and the Leu at position 11 in the wild-type have been crossition 12 in the wild-type have been crossition 20 are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with and canti-resorptive therapy (bisphosphonates and calcitonin).

CL N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications cross stated in the claim.
                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 W09702834-A1.
30-JAN-1997;
03-JUL-1996; U11292.
11-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
Dong ZX;
WPI; 97-118819/11.
New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and broam fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture. Homo sapiens.
Synthetic.
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12 gkhlnsm 18
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1 GKHLNSM 7
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/note= "Cha"
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "In amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Cyclohexylalanine (Cha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label- OTHER
                                                               Score 51; DB 22; Length 34; Pred. No. 1.10e+01; 0; Mismatches 0; Indels
                                                                                               Length 34;
                                                                  0;
                                                                  Gaps
                                                                  0
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Arch completed: Thu Jul 30 10:20:20 1998 ob time : 18 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:19:17 1998; MasPar time 3.25 Seconds 78.689 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-10 (1-7) from US08817547A.pep 51 1 GKHLNSM 7

Description: Perfect Score: Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 19.845; Variance 21.817; scale 0.910

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

NO.
Score
Match
Match Length
BB
Ü
Description
Pred. No.
51 100 0 34 5 1955 parathropold homoso / 0 /10-03

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24
37	37	37	37	37	37	38	38	38	38	38	38	38	39	39	39	39	39	39	39	39	39
72.5			72.5			74.5				74.5		74.5		76.5						76.5	
491	295	295	295	253	193	670	545	290	193	181	176	152	662	648	587	437	437	377	356	318	263
N	ഗ	ر.	v	ب	N	N	2	N	N	N	N	N	2	N	N	ν	N	N	N	N	N
140991	2AT2C	2AT2B	2AT2A	MYUHMA	E69469	S47042	E69907	A36134	A53835	A64393	S22310	S22311	S61193	A64167	S61038	S48853	S52014	S61892	S39889	F38888	в69807
signal transducer amp	Aspartate transcarbam	Aspartate transcarbam	Aspartate transcarbam	phosphoglycerate muta	hypothetical protein	protein kinase (EC 2.	DNA recombinase homol		SEC63 protein complex	hypothetical protein	HMG-Y-related protein	HMG-Y-related protein	probable membrane pro	cyck protein homolog	D-lactate dehydrogena	H+-transporting ATP s	atp6 protein - common	outer membrane protei	SMR1 protein - Podosp	COI intron 13 protein	polysaccharide deacet
1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02	9.24e+01	9.24e+01	9.24e+01	9.24e+01	9.24e+01	9.24e+01	9.24e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01

ATE_NAMES TLE SM NCE NCCE bmission coss-referen thors	Db 12 GKHLNSM Qy 1 GKHLNSM	Query Match Best Local Similarity Matches 7; Conse	19-30 SUMMARY	rs	E Ors ission s-referen E	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM
lzwE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 rces PDB:1ZWE TN001721 MATX, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	d 18	100.0 100.0 rvativ	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR . hormone	Marx, U.C. the Brookhave	12WA #type complete parathyroid hormone (residues 1-34) - human HTH(1-34) HTHUCTURE of human parathyroid hormone fragment 1-34, NMR 10 structures #formal_name Homo sapiens #common_name man

	arch co	COMMENT Resolution: not applicable COMMENT Determination: NMR KEYWORDS hormone 15-25 \$#region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4128 #checksum 5508 Query Match Best Local Similarity 100.0%; Score 51; DB 5; Length 34; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 9 GKHLNSM 15 Ov 1 GKHLNSM 15 Ov 1 GKHLNSM 15

***************** (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:17:47 1998; MasPar time 2.06 Seconds 85.162 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-10 (1-7) from US08817547A.pep 51 1 GKHLNSM 7

Sequence:

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 20.740; Variance 18.384; scale 1.128

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score 51	ery tch	Length	1 : B	ID PTHY_HUMAN PTHY BOVIN	HORMONE	Pred. No.
ωκ	47	92.2	115	ہر مر	PTHY_BOVIN	(A) (E)	1.19e-01
4	44	86.3	2105	Ь	POLR_ASGVP	GENOME POLYPROTEIN (CN	8.38e-01
5	42	82.4	501	\vdash	YBQ6_YEAST	HYPOTHETICAL 57.8 KD P	2.92e+
o	41	80.4	558	\vdash	YGZB_YEAST	64.9 KD	5.37e+00
7	41	80.4	3005	_	ZFH2_DROME	ZINC-FINGER PROTEIN 2	5.37e+00
œ	40	78.4	115	Н	PTHY_PIG	PARATHYROID HORMONE PR	9.74e+00
Q	40	78.4	373	سر	LEF3_NPVOP	LATE EXPRESSION FACTOR	9.74e+00
10	40	78.4	465	,	FTSW_MYCLE	PROBABLE CELL DIVISION	9.74e+00
11	40	78.4	601	μ	YAN4_SCHPO	HYPOTHETICAL 69.4 KD P	9.74e+00
12	40	78.4	690	H	LIP_STAAU	LIPASE PRECURSOR (EC 3	9.74e+00
13	39	76.5	176	ب	PACA_HUMAN	PITUITARY ADENYLATE CY	1.75e+01
14	39	76.5	356	μ	SMR1_PODAN	SPORULATION MINUS REGU	1.75e+01
15	39	76.5	377	۳	AMSH_ERWAM	AMYLOVORAN EXPORT OUTE	1.75e+01
16	39	76.5	587	_	DLD1_YEAST	D-LACTATE DEHYDROGENAS	1.75e+01
17	39	76.5	648	Н	CCMF_HAEIN	CYTOCHROME C-TYPE BIOG	1.75e+01
18	39	76.5	. 662	щ	PMT7_YEAST	DOLICHYL-PHOSPHATE-MAN	1.75e+01
19	38	74.5	152	Ц	HMGB_SOYBN	HMG-Y RELATED PROTEIN	3.09e+01
20	38	74.5	176	Н	HMGA_SOYBN	HMG-Y RELATED PROTEIN	
21	38	74.5	192	<u>س</u>	SC72_YEAST	TRANSLOCATION PROTEIN	3.09e+01
22	38	74.5	204	_	IL1A_CAVPO	INTERLEUKIN-1 ALPHA PR	3.09e+01
23	38	74.5	469	Н	FTSW_MYCTU	PROBABLE CELL DIVISION	3.09e+01

454	43	42	41	40	39	38	37	36	3	34	ယ ယ	32	31	30	29	28	27	26	25	24
37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	38
72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	74.5
2364	985	931	756	709	700	692	642	514	491	478	430	415	404	384	281	252	208	174	142	470
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SPCO_HUMAN	NAH_YEAST	DING_BACSU	MAOX_HAEIN	MBA2_ECOLI	PTPE_HUMAN	YYI3_CAEEL	SYT_ECOLI	LIM_HALRO	AMPG_ECOLI	YDD2_SCHPO	DFP_ECOLI	THBG_HUMAN	Y432_MYCPN	Y039_MYCPN	P2C1_YEAST	PMGM_RAT	YFJJ_ECOLI	FRIL_RABIT	HBA3_PLEWA	LEU2_AZOVI
SPECIRIN BETA CHAIN, B	(+) AN	PROBABLE ATP-DEPENDENT	PUTATIVE MALATE OXIDOR	MOBILIZATION PROTEIN A	PROTEIN-TYROSINE PHOSP	PROBABLE G PROTEIN-COU	THREONYL-TRNA SYNTHETA	HOMEOBOX PROTEIN LIM (AMPG PROTEIN.	HYPOTHETICAL 55.4 KD P	DNA/PANTOTHENATE METAB	THYROXINE-BINDING GLOB	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	PROTEIN PHOSPHATASE 2C	PHOSPHOGLYCERATE MUTAS	HYPOTHETICAL 24.6 KD P	FERRITIN LIGHT CHAIN.	HEMOGLOBIN ALPHA CHAIN	3-ISOPROPYLMALATE DEHY
5.38e+01		5.38e+01	5.38e+01	5.38e+01		5.38e+01	٠	٠			5.38e+01	5.38e+01	5.38e+01	5.38e+01	5.38e+01		5.38e+01	5.38e+01	5.38e+01	•

RRERE	RAR	R R	RA	RP	R R	RA P	RX	R R	RE S	0 X	RP	R F	RA	RA A	R RP	R P	RA	RX	R R	8	88	o o	DE	DI	7 7	AC	RESULT
O'RICKDAN J.L.H., FOITS J.T. JR.; (IN) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975). [7]	O. ALL H.I	BIOCHEMISTRY 17:5723-5729(1978).	AN.	SEQUENCE OF 61-83 AND 84-115.	SCI. U.S.A. 71:384-388(1	NIALE H.D., SAUER R.T., JACOBS J.W., RECIMANN H.T., SEGRE G.V.,	111656.	[4]		TW KEMDER B NIALL H D HARENER T.F	SEQUENCE OF 26-37.	SC1. U.S.A.	G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;	VASICEK T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J.,	SEQUENCE FROM N.A.	700	G.N., KRONENBERG H.M.	NE; 82150870.	SEQUENCE FROM N.A.	PRIMATES.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	SNALGES	THYROID HORMON	35, LAST ANNOTATIO	13-AUG-1985 (REF. OI, CREATED)	:	SULT 1 PTHY_HUMAN STANDARD; PRT; 115 AA.

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SO PITT FITTERS OF THE FITTERS OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
RA KRONENBERG H.M.;

RI J. CLIN. INVEST. 86:1084-1087(1990).

CC :- FUNCTION: PTH BLEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

CC BONE AND PREVENTING THEIR RENAL EXCRETION.

CC HYPOPARATHYROIDISM (FIH).

CC HYPOPARATHYROIDISM (FIH).

CREMEL; J00301; G190704; -...

CREMEL; J00301; G190704; -...

CREMEL; V00597; G37144; -...

CREMEL; V00597; G37144; -...

CREMEL; J01339, A19339.

PDB: 11HH; 10-JUL-95.

PDB: 11HH; 10-JUL-95.

PDB: 11HH; 10-JUL-95.

PDB: 11ZWA; 112-MAR-97.

CREMEL; LUWA; 12-MAR-97.

CREMEL; LUWA; 12-MAR
    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRÚCTURE BY NMR OF 32-68.
MEDLINE; 95318084.
MARX U.C., AUSTERMANN S., B
STICHT H., WALTER S., SCHMI
ROESCH P.;
                                                                                                                                                                      CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 32-65
MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON |
EUR. J. BIOCHEM. 215:315-
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MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTT.
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLAUS W., DIECKMANN T., WRAY V., BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 32-65 MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WI
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MEDLINE; 73227467.

ANDREATTA R.H., HARTMANN A., JOEHL
RINIKER B., RITTEL W., SIEBER P.;

HELV. CHIM. ACTA 56:470-473(1973).
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MEDLINE: 75146516.

KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T.

BIOCHEMISTRY 14:1842-1847(1975).
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MEDLINE; 91009811.
                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HORMONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOL.
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SIGNAL; D
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115
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HEM. 215:315-321(1993).
                                                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PARATHYROID; 1. DISEASE MUTATION;
                                                                                                                                                                  107
12861
                                                                                                                                                                                                                                                                                       31
115
18
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                                                                                                                                                                           MW;
                                                                                                                                                      PARATHYROID HORMONE.
C -> R (IN FIH; LEADS
PROCESSING OF THE PRE
N -> D (IN REF. 5).
W; 243E87C7 CRC32;
Score 51; DB 1; Pred. No. 7.72e-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-STRUCTURE
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JAENICKE
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                                                                                                                                                                                                                                                 PRECURSOR)
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FORSSMANN
    Indels
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    Gaps
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RESULTATION OF THE PROPERTY OF
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                                                                                         BONE AND PREVENTING THEIR RENAL EXEMBL; V00106; G85; -. EMBL; J00023; G163641; -. EMBL; J00024; G163643; -. EMBL; J00024; E18849; ALT_SEQ. EMBL; J00024 E18250; ALT_INIT. EMBL; K01938; G163647; -.
                                                                         EMBL; J00024;
EMBL; J00024;
EMBL; J00024;
EMBL; J00024;
EMBL; K01938;
EMBL; K01938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 8310
WEAVER C.A.,
MOL. CELL. EN
                   PIR; A249
PROSITE;
                                                                                                                                                                                                         MEDLINE; 71091588.

POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D. DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.; PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986
21-JUL-1986
01-NOV-1997
                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 32-115.
MEDLINE; 71076162.
NIALL H.D., KEUTMANN H.T.,
AURBACH G.D., POTTS J.T. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.
COHN D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
WEAVER C.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRONENBERG H.M., MCDEVITT B.E POTTS J.T. JR., RICH A.; PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTH.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 32-115. MEDLINE; 71063634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 82037785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 80056617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOS TAURUS EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTHY_BOVIN P01268;
                                                                                                                                                                                                                                                                                                                             SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOPPE-SEYLER'S Z. PHYSIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARATHYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43
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                                       A24949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NATL.
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71091588.
   SIGNAL.
                   PS00335;
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A., GORDON
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METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAD. SCI.
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(REL. 01, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH)
                                     A24949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GORDON D.F.,
                                                                         G163645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCI.
                   PARATHYROID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.F., KEMPER B.;
OL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                 U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JR.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KISSIL M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEMPER B.;
3.A. 78:4073-4077(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAUER R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JACOBS
                                                                                                                                                                                                                                                                                                                                                               67:1862-1869(1970)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAJZOUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                             351:1586-1588(1970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOGAN M.L., DAWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEAD D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEUTMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEMPER
                                                                                                                                                                                                                                                                                       H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.,
                                                                                                                                                                                                                                 THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B.F.,
                                                                                                                                                                                                                                                                                       SAUER
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                                                                                                                                                                                                                                 SALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.T.
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KIAA0361 (FRAGMENT).	RNA POLYMERASE (FRAGME	NUCLEOSIDE TRIPHOSPHAT	G3R PROTEIN.	CHITINASE.	PROSAPOSIN.	CHROMOSOME XV READING	HYPOTHETICAL PROTEIN.	SULFIDE-DEHYDROGENASE	PUTATIVE - POSSIBLE PH	HYPOTHETICAL 22.0 KD P	PARATHYROID HORMONE (F	UVRB (FRAGMENT).	SIMILARITY TO MULTIPLE	HYPOTHETICAL 140.5 KD	ATED PROTE	CATALASE (EC 1.11.1.6)	M04G12.3.	YOKA PROTEIN.	HYPOTHETICAL 52.6 KD P	ALPHA-AMYLASE.	MOBILIZATION PROTEIN.	HYPOTHETICAL 36.4 KD P	REPLICATION PROTEIN A	HYPOTHETICAL 21.1 KD P
	٠.		•	6.49e+01	6.49e+01		•	•	•	6.49e+01	6.49e+01	6.49e+01	•	•	•	3.69e+01		'n		3.69e+01	:	٠	3.69e+01	

ALIGNMENTS

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RESULT
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1012828
1012828
101-NOV-1996 (TREMBLREL. 01, CREATED)
101-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
101-NOV-1996 (TREMBLREL. 01, CREATED)
101-JUL-1997 (TREMBLREL. 04, CREATED)
101-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

101-NOV-1996 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
101-NOV-1996 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
101-NOV-1996 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
101-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

101-NOV-1996 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

101-NOV-1996 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
101-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

101-NOV-1996 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

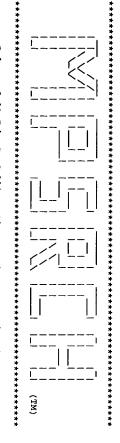
101-NOV-1996 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
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Search completed: Thu Jul 30 10:18:58 1998 Job time: 45 secs.
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RA BOURLET E., ORASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA BOURTSER L., BERSIERES P., BOLOTIN A., BORCHERT S.,
RA BOURLET S., BRUSCIEL C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J. DANKER R.
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J. DANKER R.
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J. DANKER R.
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J. DANKER R.
RA CHIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA CHIZOC., FUJITA M., FUJITA Y., FUMA S., GALLIZZI A., GALLERO N.,
RA CHIZ C., FUJITA M., FUJITA Y., FUMA S., GALLIZZI A., GALLERO N.,
RA CHIZ S.Y., GLASER P., GOFERAU A., GCLIGHTLY E.J., GRANDI G.,
RA GHIM S.Y., CLASER P., GOFERAU A., GCLIGHTLY E.J., GRANDI G.,
RA GHIM S.Y., CLASER P., GOLTER P., KONINGSTEIN G., KROCH S., KUMANO M.,
RA GUISEPPI G., GUY B.J., HAGA K., HALECH J., HARMOOD C.R., HERNUT A.,
RA KURITA K., LAPIJUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIJUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIJUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA MEDIKA N., MELLADO R.P., MIZUNO M., MOESTL D., MAKAI S., NOBACK M.,
RA PARRO V., POHL T.M., PORTETELLE D., PORMOLLIK S., PRESCOTT A.M.,
RA RIBGER M., RIVOLTA C., ROCHA E., ROCHA E., ROSEM M., REYNOLDS S.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOPFONE F.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOPFONE F.,
RA AKEUCHI M., TAMAKOSHI A., TANAKA T., TERESTRA P., TOGNONI A.,
RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERESTRA P., TOGNONI A.,
RA TAKEUCHI M., TAMANOTO H., YANANE K., YASSAROTTI A.,
NATURES P., WEDLER E., WEDLER H., WEJTZENBEGER T.,
NATURES 90:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches
                                                                                                                                                                                                                              KUNST F. OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; D88802; D1020491; -.
EMBL; 299107; E1182567; -.
SEQUENCE 362 AA; 40834 MW; 616962F9 CRC32;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-168;
                                                                                                                      162 GKRLNAM 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-168;
SADAIE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
OGASAWARA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SADAIE Y., YA
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                                                                                1 GKHLNSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) BACILLUS SP. MANNAN ENDO-1.
                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
                                                                                   7
                                                                                                                                                             Conservative
                                                                                                                                                                                 82.48;
                                                                                                                                                      Score 42; DB 9; L
Pred. No. 3.42e+00;
2; Mismatches 0
                                                                                                                                                                                              Length 362,
                                                                                                                                                        0
                                                                                                                                                    Indels
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                                                                                                                                                    Gaps
                                                                                                                                               0;
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Psrch_pp 9 2: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:22:22 1998; MasPar time 2.66 Seconds 34.605 Million cell upda

updates/sec

Description: Perfect Scor Title: Score: (1-6) from US08817547A.pep 44 1 KHLNSM 6 >US-08-817-547A-11

Tabular output

not generated

Scoring table: Sequence: PAM 150 Gap 15

124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.509; Variance 37.219; scale 0.363

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11111111111111111111111111111111111111	Result
242442444	Score
	- Ch.7
20 20 20 20 20 20 20 20 20 20 20 20 20 2	Length D
222222	DB ID
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	D
Human parathyroid hor Gln25,26,27]hPTH (1-Target peptide (PTH(1 N-alpha-Isopropyl-hPTH Human parathyroid hor Human parathyroid hor Human parathyroid hor Human parathyroid hor [Ala]-hpTH(1-36)-NH2 [Cha8]-hPTH(1-36)-NH2 [Cha8]-hPTH(1-36)-NH2 [D-Val31]-hPTH(1-36)-NH2 [D-Val31]-hPTH(1-36)-NH2	Description
4.47e+01 6.47e+01 6.47e+01 6.47e+01	Pred. No.

Query Match

100.0%;

Score 44; ВВ 22;

Length

34

44 100.0 38 9 RS8147 [His21]-hPTH(1-38)-OH 44 100.0 38 9 RS8147 [His22]-hPTH(1-38)-OH 44 100.0 38 9 RS8147 [Pro19]-hPTH(1-38)-OH 44 100.0 38 9 RS8132 [Pro19]-hPTH(1-38)-OH 44 100.0 38 19 RS8132 [Pro19]-hPTH(1-38)-OH 44 100.0 38 19 RS8132 [Pro19]-hPTH(1-38)-OH 44 100.0 44 26 P30015 Human parathyroid hor 44 100.0 47 25 WZ1946 FUSION protien compri 44 100.0 84 6 R30859 Leaß hPTH muttein lacking 3 44 100.0 84 4 RZ1210 Human parathyroid hor 44 100.0 84 4 RZ3232 Human parathyroid hor 44 100.0 84 4 RZ3232 Human parathyroid hor 44 100.0 84 4 RZ3233 Human parathyroid hor 44 100.0 84 4 RZ3233 Human parathyroid hor 44 100.0 84 4 RZ1219 Human parathyroid hor 44 100.0 84 4 RZ1216 Human parathyroid hor 44 100.0 84 4 RZ1161 Human parathyroid hor 44 100.0 84 4 RZ1161 Human parathyroid hor 44 100.0 84 4 RZ1161 Human parathyroid hor 44 100.0 84 4 RZ1153 Human parathyroid hor 44 100.0 84 4 RZ1218 Human parathyroid hor
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9 R58141 [Leu21]-hPTH(1-38 9 R58147 [His22]-hPTH(1-38 9 R58132 [Pro19]-hPTH(1-38 9 R58132 [Pro19]-hPTH(1-38 19 R58132 [Pro19]-hPTH(1-38 11 R98958 Target peptide (P 26 P30015 Human parathyroid 25 W21946 Fusion protien co 6 R30859 hPTH (7-84) 6 R30854 hPTH mutein lack! 27 W25687 Human parathyroid 4 R231210 Human parathyroid 4 R23332 Human parathyroid 4 R23335 Human parathyroid 4 R23235 Human parathyroid 4 R231209 Human parathyroid 4 R21160 Human parathyroid 4 R21161 Human parathyroid 4 R21123 Human parathyroid 4 R21124 Human parathyroid 4 R211254 Human parathyroid 4 R211254 Human parathyroid 4 R21218 Human parathyroid 4 R21218 Human parathyroid 4 R23237 Human parathyroid 4 R23237 Human parathyroid 4 R23237 Human parathyroid 4 R23133 Human parathyroid
R58141 [Leu21]-hPTH(1-38 R58147 [His22]-hPTH(1-38 R58128 [Met19]-hPTH(1-38 R58128 [Met19]-hPTH(1-38 R58128 [Pro19]-hPTH(1-38 R58132 [Pro19]-hPTH(1-38 R58132 [Pro19]-hPTH(1-38 R58132 [Pro19]-hPTH(1-38 R58132 [Pro19]-hPTH(1-38 R58132 [Pro19]-hPTH mutein co R30859 Leu8 hPTH mutein lacki R30859 hPTH mutein lacki R31210 Human parathyroid R23232 Human parathyroid R23232 Human parathyroid R23233 Human parathyroid R23523 Human parathyroid R23523 Human parathyroid R21253 Human parathyroid R21160 Human parathyroid R21161 Human parathyroid R21218 Human parathyroid R21218 Human parathyroid R23231 Human parathyroid R23233 Human parathyroid R23233 Human parathyroid R23233 Human parathyroid R23233 Human parathyroid R23123 Human parathyroid R23133 Human parathyroid R23133 Human parathyroid R23133 Human parathyroid
[Leu21] -hPTH(1-38 [Hi322] -hPTH(1-38 [Met19] -hPTH(1-38 [Pro19] -hPTH(1-38 [Pro19] -hPTH (1-38 [Pro19] -hPTH mutein protien co Leuß hPTH mutein lacki human parathyroid
12] -hpTH(1-38 [2] -hpTH(1-38 [9] -hpTH(1-38 [9] -hpTH(1-38 et peptide (P parathyroid nprotien con hpTH (7-84) hpTH (7-84) mutein lacki parathyroid

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33-JUL-1996; U11292.

13-JUL-1995; US-001105.

06-SEP-1995; US-003305.

29-MAR-1996; US-626186.

29-MAR-1996; US-626186.
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Human parathyroid hormone analogue [Nle31]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
and calcitonin).

N.B. The present sequence does not appear in the corresponds to the known hPTH 1-34 fragment with as stated in the claim.

Sequence 34 AA;
                                                                                                                                                                               Claim 20; Page -; 33pp; English.

The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least the amino acid residue at position 1 is alpha, beta-diaminopropionic acid, the amino acid residue at position 27 is homoarginine, or the amino aci residue at position 27 is homoarginine, or the amino aci residue at position 31 is norleucine. In this example the Val residue at position 31 in the wild-type has been substituted by Nle. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates optionally in conjunction with anti-resorptive therapy (bisphosphonates)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stimulate bone growth
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New variants of human
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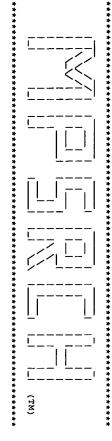
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RESULT
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                                                                                                                                                                           To bone fracture

1 Schalm 5; Page -; 33pp; English.

2 Claim 5; Page -; 33pp; English.

2 The present sequence is a specific example of a human parathyroid of hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 of is cyclohexylalanine (Cha). In this example the Leu residue at position 7 and the Leu at position 11 in the wild-type have been of substituted by Cha. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).

2 N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim.
                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
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Matches 6; Conservative
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03-JUL-1996; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.
Synthetia
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W17939 standard; peptide; 34
W17939;
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WPI; 97-118819/11.
New variants of human parathyroid hormone 1-34 peptide - which
stimulate bone growth and are used for treatment of osteoporosis
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                                                             KHLNSM 6
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11
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Pred. No. 4.47e+01;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

92: Thu Jul 30 10:21:36 1998; MasPar time 3.04 Seconds 72.203 Million cell updates/sec

fabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-11 (1-6) from US08817547A.pep 44 1 KHLNSM 6

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 18.883; Variance 20.866; scale 0.905

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

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1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01						

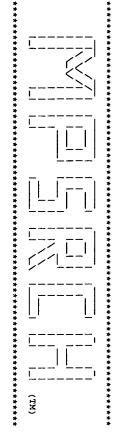
RESULT 2 12W ENTRY TITLE PARTS HPTT ALTERNATE_NAMES HPTT PDB_TITLE STT ORGANISM #fo. REFERENCE #671 # authors Roel # cross references REFERENCE # Sub # cross references REFERENCE TNO # authors Mar: # book PD	Query Match Best Local Sim Matches 6; Matches 13 KHLNSM Qy 1 KHLNSM	FEATURE 6-9 19-30 SUMMARY	hors k	ORGANISM #formal_name REFERENCE A67856 #authors Roesch, P.; #submission submitted to #submission FDB:12WA	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
12WE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 ces PDB:1ZWE TN001721 MATX, U.C. MATX, U.C. In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	h 100.0%; Score 44; DB 5; Length 34; Similarity 100.0%; Pred. No. 2.07e+00; 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; LNSM 18	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	MATX, U.C. MATX, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR hormone	#formal_name Homo sapiens #common_name man A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 soes PDB:IZWA	12WA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures

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COMMENT COMMENT RESOlution: NMR
KEYWORDS
FRATURE
15-25
#region belix (right hand alpha)
SUMMARY

Guery Match
Best Local Similarity 100.0%; Score 44; DB 5; Length 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 KHINSM 15
Qy 1 KHINSM 6

Search completed: Thu Jul 30 10:22:04 1998
Job time: 28 secs.
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Psrch_pp <u>8</u> protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:20:37 1998; MasPar time 2.04 Seconds 73.747 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-11 (1-6) from US08817547A.pep 44 1 KHLNSM 6

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 19.767; Variance 17.440; scale 1.133

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 41 93.2 3005 1 2FH2_DROME 4 40 90.9 115 1 PTHY_GOVIN 5 40 90.9 115 1 PTHY_CANEPA 6 40 90.9 373 1 LEES_NPONE 6 40 90.9 373 1 LEES_NPONE 7 39 886 662 1 PMT7_YEAST 8 37 84.1 208 1 YFJJ_ECOLI 9 37 84.1 252 1 PMGM_HUMAN 11 37 84.1 252 1 PMGM_HUMAN 12 37 84.1 384 1 YO39_MYCDL 13 37 84.1 384 1 YO39_MYCDL 13 37 84.1 384 1 YO39_MYCDL 14 37 84.1 430 1 DFP_ECOLI 15 37 84.1 438 1 YDJ2_SCHPOC 17 37 84.1 478 1 YDJ2_SCHPOC 17 37 84.1 491 1 AMPG_ECOLI 18 37 84.1 491 1 AMPG_ECOLI 19 37 84.1 648 1 NTPJ_CBEPN 19 37 84.1 648 1 NTPJ_CBEPN 20 37 84.1 692 1 YYI3_CAEBL 21 37 84.1 931 1 DING_BACSU 22 37 84.1 931 1 DING_BACSU 23 36 81.8 101 1 YGF2_YEAST				. L L B	ID PTHY_HUMAN POLR_ASGVP	HORMONE PROTEIN (
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7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01

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(IN) CALCIUM-REGILATING HORMONES, TALMADGE R.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975). [7]	O. ALL H.E	BIOCHEMISTRY 17:5723-5729(1978).	KEUTMANN 1902003. KEUTMANN 11., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,		O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.; PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).	R.T., JACOBS J.W., I	SEQUENCE OF 32-68.	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.; NATURE 249:155-157(1974).	E; 74174967.	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).	G.N., POTTS J.T. JR., RI	E FROM N.A.	ACAD. SCI. U.S.A.	82150870. N., KRONENBERG H.M., POTTS J.T	SEQUENCE FROM N.A.	ARYOTA; ME HERIA; PRI	HOMO SAPIENS (HUMAN).	HORMONE PRECURSOR (PARATH)	(REL. 05,	21-JUL-1986 (REL. 01, CREATED)	ULT 1 PTHY HUMAN STANDARD; PRT; 115 AA.

JR.;

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SETT THE SET OF SETTINGS
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Best Local Similarity 100.0%;
Matches 6; Conservative
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PIR: A19339; A19339;
PDB: 1HPH: 10-7UL-95;
PDB: 1HTH: 15-OCT-97;
PDB: 1ZWA: 12-MAR-97;
PDB: 1ZWC: 16-JUN-97;
                                                 CONFLICT
SEQUENCE
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EMBL; V00597;
EMBL; A29146;
                                                                                                 PROPEP
CHAIN
                                                                                                                                    PROSITE;
HORMONE;
                                                                                                                                                                                                                                                                                                                                                ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A., KRONENBERG H.M.;

J. CLIN. INVEST. 86:1084-1087(1990).

-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS BONE AND PREVENTING THEIR RENAL EXCRETION.

-I- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED HYDODARAHYROLDISM (FIH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 32-68.
MEDLINE; 95318084.
MARX U.C., AUSTERMANN S.,
STICHT H., WALTER S., SCHM
ROESCH P.;
                                                                                     VARIANT
                                                                                                                          SIGNAL
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EUR. J. BIOCHEM. 215:315-321(1993).
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MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON 1
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MEDLINE: 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 91009811.
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TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D. KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J. HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE; 75146516.

KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T.
BIOCHEMISTRY 14:1842-1847(1975).
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MEDLINE; 73227467.
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12-MAR-97.
16-JUN-97.
16-JUN-97.
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115
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SCHMID F.-X.,
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Score 44; DB 1; I
Pred. No. 3.21e-01;
0; Mismatches 0
                                            PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEF
PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
1; 243E87C7 CRC32;
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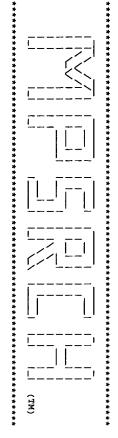
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RESULT 2

ID POLR ASGVP STANDARD; PRT; 2105 AA.
AC P36309;
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE (EC.)
COAT PROTEIN.

COAT PROTEIN (CONTAINS: RNA REPLICASE)
COAT PROTEIN (SITRAIN P-209) (ASGV).
CO VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CAPILLOVIR.
RN SEQUENCE FROM N.A.
RN MEDLINE; 93033164.
RN MEDLINE; 944059; G285608; -.
PIR; A44059; A4405
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Pred. No. 3.21e-01;
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Search completed: Thu Job time: 7 secs. secs. Jul 30 10:20:44 1998



MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 10:21:01 1998; MasPar time 3.61 Seconds 69.980 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-817-547A-11 (1-6) from US08817547A.pep 44 1 KHLNSM 6

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fug1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mbc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 18.888; Variance 17.056; scale 1.107

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11331111111111111111111111111111111111	Result No.
34444 338 338 337 377 377	Score
88888888888888888888888888888888888888	Query Match
719 3703 3726 4211 315 367 545 545 545 545 545 545 545 545 545 54	Length
82211 82218 83218	B
Q17828 Q15911 Q15911 Q61329 Q61329 Q61329 Q451528 Q21523 Q45125 Q232006 P92006 P92006 P92539 Q28516 Q28516 Q285177 Q35690 Q461770 Q461770 Q461770 Q461775 Q46175	Ü
COSFS.2. ZINC ETMGER HOMEODOMAI ZINC ETMGER HOMEODOMAI AT MOTIF BINDING FACTO YRVN PROTEIN. HYPOTHETICAL 36.4 KD P MOBILIZATION PROTEIN. YOKA PROTEIN. MO4G12.3. CATALASE (EC 1.11.1.6) UNKNOWN PROTEIN (FRAGM HYPOTHETICAL 22.0 KD P TRANSPOSON TN5405 AND PUTATIVE - POSSIBLE PH COXI INTRON 1 ORF. CHROMOSOME XV READING ALPHA-AMYLASE. MCM2-RELATED PROTEIN (PROSAPOSIN.	Description
1.30e+00 2.48e+00 2.48e+00 4.68e+00 1.60e+01 1.60e+01 1.60e+01 1.60e+01 1.60e+01 1.60e+01 1.60e+01 2.91e+01	Pred. No.

443	441 421	3 3 3 9 8	36 37	ω ω 4 7	33	3 3 2 1	30	28 29	27	26	25	24	23	22	21
333	ა	366	3 B	<u>თ</u> თ	36	ພ ຜ ດ	36	თ თ თ	36	37	37	37	37	37	37
79.5 79.5 79.5										84.1		84.1		84.1	84.1
1642 12 3410 11 3410 11	2343 . 334 1:									3429					585 11
	Q9046			Q1466 Q2257				9 024682 8 041320		Q2459	Q2366	03915	03731	1 08909	1 00704
01000					σ .	ro 4	7			ω	·	7	v	7 G	0
22	FACTOR VIII. HER-6 PROTEI	C06B3.8.	DNA-BINDING AMYLOID BET	BINDING PROT ACETOLACTATE		ASPARTATE CARBAMOYLTRA BINDING PROTEIN (FRAGM	ENDONUCLEASE	COLICIN	HOST SHUT	X GENE.	ZK930.1.	MYOSIN (NUCLEOSIDE	GARCIA-1966	G3R PROTEIN
	H · و		≫	- 12		TE CARBAI	EASE III	U IMMUNITY	OFF			(FRAGMENT)	DE TRIP	966 RIGHT	EIN.
FACTOR PRE	. TROIBLN.	4) PREC	PROTEIN (F	SYNTHASE.	PROTEIN, F	MOYLTRA (FRAGM	I (NTH)	NT FOR	9				TRIPHOSPHAT	HT NEAR	
9.25e+01 9.25e+01 9.25e+01	5.23e+01 9.25e+01	5.23e+01 5.23e+01				5.23e+01		5.23e+01 5.23e+01	٠	2.91e+01	io	٠		2.91e+01	
222	222	222	22	21	21	22	21	ឧឧ	2	21	21	21	01	01	입

RESULT ID O AC O DT 0	уру Ма Ве	TREASON SERVING CONTRACTOR OF THE COLOR OF T
JLT 2 015101 015101; 01-JAN-1998 01-JAN-1998	Query Match Best Local Simi Matches 5; 638 KHLDSM 1 KHLNSM	17828; 17828; 1-NOV-19; 1-
PRELIMINARY; (TREMBLREL. 05, (TREMBLREL. 05,	95.5%; Similarity 83.3%; 5; Conservative CLDSM 643 :	PRELIMINARY; PR 1996 (TREMBLREL 01, CREA 1996 (TREMBLREL 01, LAST 1996) TO EMBL/GEN 1994150718 19941507
Y; PRT; 1072 AA. 5, CREATED) 5, LAST SEQUENCE UPDATE)	; Score 42; DB 3; Length 719; ; Pred. No. 1.30e+00; 1; Mismatches 0; Indels 0; Gaps 0;	Q17828 Q17828;

```
DE ZINCE FINGER HOMEODOMAIN PROTEIN (3' PARTIAL) (FRAGMENT).

OS HOMO SAPIENS (HUMAN).

OC EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

RI (1)

RP SEQUENCE FROM N.A.

RA ADAMS M.D.; LOFTUS B.J.; ZHOU L., LABOMBARD M., FUHRWANN J.,

RA BRANDON R.; KIM U.J.; KERLAVAGE A.R.; VENTER J.C.;

DR EMBL; ACO02044; C234708; -

EMBL; ACO02044; C234708; -

SO SEQUENCE 1072 AA; 115896 MW; 78611913 CRC32;

Ouery Match
Best Local Similarity 83.3%; Pred. No. 2.48e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps

749 KHLNNM 754

IIII:

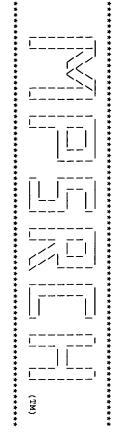
ITHER 1072

ITHER 1072

ITHER 1072

Search Completed: Thu Jul 30 10:21:19 1998

Search Completed: Thu Jul 30 10:21:19 1998
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

h on: Thu Jul 30 10:24:45 1998; MasPar time 2.51 Seconds 30.581 Million cell updates/sec Tabular output not generated.

Title: >US-08-817-547A-12
Description: (1-5) from US08817547A.pep
Perfect Score: 37
Sequence: 1 HLNSM 5

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.437; Variance 34.377; scale 0.362

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 110 110 110 110 110 110 110 110 110	<u>۔</u> ا	Result
30 30 30 30 30 30 30 30 30 30 30 30 30 3	37	Score
	100.0	Query Match
	28	Length
9 9 222 222 222 4 4 4 7 7 7 7 7 7 7 7 7 7 7	4	BB
R58188 W17948 W17938 W17939 W17939 W17955 W17954 W17959 W17969 W17969 W17969 W17969 W17969 W17969 W17969 W17969 W17969 W17943 W1794 W17943 W17	R22066	ID
Parathyroid antagonis [F23,H26,L27,T28, Human parathyroid hor Human PH derivative, [Phe23]-hPTH(1-36)-NH [D-ASN33]-hPTH(1-36)	Modified [D-Trp_12Tyr	Description
1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02 1.89e+02	1.89e+02	Pred. No.

Query Match 100.0%; Best Local Similarity 100.0%; Matches 5; Conservative

Score 37; DB 4; Length 28; Pred. No. 1.89e+02; 0; Mismatches 0; Indels

0

Gaps

0

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	
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4	84 4	4	4	4	4	84 4	4	4	4	84 4	4	7	4	38 9	œ	œ	œ	œ	œ	σ	σ	σ	σ	σ	c
R21	R21	R21	R21154	R2115	W294		R212	R212		R212		W2194	P3001		R989	R5815	R58	R581	R5813		R58278	R582	R582	R582	7
	n parathyroid	Human parathyroid hor		Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Fusion protien compri	Human parathyroid hor	[Val19]-hPTH(1-38)-OH	Target peptide (PTH(1	[Arg26]-hPTH(1-38)-OH)]-hPTH(1	7]-hPTH(1-	[Gly21]-hPTH(1-38)-OH	[D-Leu15]-hPTH(1-36)-	PTH (1-3	_glycin1]-h	1-36)	Asn16]-hPTH(1-	111/H (C)				
1.89		1.89	1.89e+02	1.89	1.89	1.89	1.89	1.89	1.89	1.89	1.89	1.89e+0	1.89	1.89	1.89	1.89	1.89	1.8	1.89	1.8	1.89	1.8	1.89e+0	. 89	F. 000

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New parathyroid hormone analogues - useful for treatment and in vitro diagnosis of PTH-dependent tumours, immune disorders, osteoporosis and hyperparathyroidism.

To steoporosis and hyperparathyroidism.

Claim 1; Column 10; 6pp; English.

The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N,N-diisobutyl or 3-phenylpropanoyl. The PTH canalogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bioactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bioassays to measure naturally occurring PTH and to diagnose the etology of or to treat osteoporosis or hypercalcaemia. It may also be used to treat hyperthyroidism and diseases caused by abberrent production therefore the substances, such as tumours. It may also be used to the production of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R22066 standard; Protein; 28 AA. R22066; R22066; 14-JUL-1992 (first entry) Modified [D-Trp_12Tyr_34]hpTH(7-34)NH2. Parathyroid hormone; analogue; osteoporosis; hyperthyroidism; tumours; hypercalcaemia; renal failure; human.
                              phase synthesis.
See also R22058-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERI ) MERCK & CO INC.
Rosenblatt M, Roubini E, Chorev M, Nutt RF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                              treat immune diseases such as inflammation. It is prepd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 92-096233/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-1990; 514394.
25-APR-1990; US-514394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5093233-A.
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   28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
/label= NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= OTHER
/note= "OTHER
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                                                                                                 by solid
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Qy Db

8 hlnsm 12 ||||| 1 HLNSM 5

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ID P40427 standard; peptide; 32 AA.

AC P40427;
D7 22-UUL-1992 (first entry)
D7 22-UUL-1992 (first entry)
D8 Parathyroid antagonist peptide.

KW Human thyroid bormone.

OS Homo saptens.

FH Key Location/Qualifiers
FT misc_difference 32
FT misc_difference 32
FT misc_difference 32
FT misc_difference 32

FT misc_difference 32

O1-SEP-1982; 150702.

O1-SEP-1982; JP-150702.

O2-SEP-1884; JP-150702.

O3-SEP-1884; JP-150702.

O3-SEP-1884; JP-150702.

O4-SEP-1982; JP-150702.

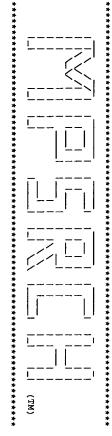
O4-SEP-1982; JP-150702.

O4-SEP-1982; JP-150702.

O5-SEP-1982; JP-150702.

O5-SEP-1982; JP-150702.

O1-SEP-1982; JP-19702.
```



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm 9 !

Thu Jul 30 10:24:01 1998; MasPar time 3.08 Seconds 59.270 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-12 (1-5) from US08817547A.pep 37 1 HLNSM 5

Scoring table: PAM 150 Gap 15

120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 17.600; Variance 17.971; scale 0.979

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2221 2322 2322 2322 2322 2322 2322 2322	Sult No.
37 37 37 37 37 37 37 37 37 37 37 37 37	Score
1000.00 1000.0	Query
34 34 34 35 35 35 35 35 35 35 35 35 35 35 35 35	Length
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	88
12WA 12WA 12WG 12WG 12WD 12WD 12WD 12WD 12WD 12WD 12WD 12WD	ij
parathyroid hormone ( parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone ( parathyroid hormone ( parathyroid hormone ( parathyroid hormone f parathyroid hormone p portection protein pypothetical protein paringenin-chalcone s	Description
1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 1.96e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01 5.87e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	4
34	34	34	34	34	34	34	34	34	34	34	34	34	35	35	35	35	35	35	35	35	Ĺ
91.9					91.9																
3005	607	594	594	593	447	396	354	346	317	232	154	151	3411	3411	1642	922	880	696	684	662	007
N	N	N	N	N	N	<b>,</b>	N	N	N	N	N	N	r	ب	N	ນ	N	N	N	N	
S33642	I37560	I58386	I56248	A47186	C64828	R3BYM1	JC1366	S62197	152575	S72439	JQ0860	F69986	GNWVY	GNWVYP	I51018	S31164	S49627	A65130	в69308	S61193	90100
homeotic protein zfh-	protein-tyrosine kina	receptor tyrosine kin	receptor tyrosine kin	receptor protein tyro	hypothetical protein	ribosomal protein var	tyrosine kinase recep	molybdenum formylmeth	gene MRK protein - mo	role	hypothetical 18K prot	acetyltransferase hom	genome polyprotein -	genome polyprotein -	cobra venom factor pr	-	regulatory protein AR	hypothetical 79.5 kD		probable membrane pro	p_ractate nemyntogena
9.99e+01	9.99e+01	9.99e+01	•	•	9.99e+01	9.99e+01	9.99e+01	9.99e+01	9.99e+01	9.99e+01	9.99e+01	9.99e+01	5.87e+01		5.87e+01	5.87e+01	5.87e+01		5.87e+01	5.87e+01	0.0/6701

ORGANISM #formal_name REFERENCE A67860 #authors Rossch, P.; #submission submitted to #cross-references PDB:12WE REFERENCE TN001721 #authors Marx, U.C. #book pp.0, Bayr	RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE	Db 14 HLNSM	Query Match Best Local Sim. Matches 5;	19-30 SUMMARY	SI	REFERENCE A671 #authors Roes #submission submission sub	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM
#formal_name Homo sapiens #common_name man A67860 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 roes PDB:1ZWE TRO01721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	12WE #type complete parathyroid hormone (residues 4-37) - human HETH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures	18	100.0%; Score 37; DB 5; Length 34; Similarity 100.0%; Pred. No. 1.96e+01; 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR hormone	A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 ICES PDB:1ZWA TN001717	12WA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures #formal_name Homo sapiens #common_name man

```
COMMENT Resolution: NMR
COMMENT EXEMPTION: NMR

EXEMPER

15-25

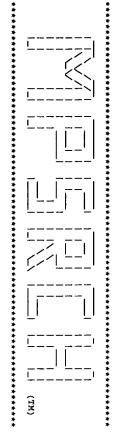
#length 34 *molecular-weight 4128 *checksum 5508

Outry Match
Best Local Similarity 100.08; Score 37; DB 5; Length 34;
Best Local Similarity 100.08; Pred. No. 1.964-01; Ength 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 HINSM 15
Cy 1 HINSM 5

Search completed: Thu Jul 30 10:24:27 1998

Job time : 26 secs.
```



Psrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:22:54 1998; MasPar time 2.01 Seconds 62.468 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-12 (1-5) from US08817547A.pep 37 1 HLNSM 5

Scoring table:

PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 18.404; Variance 15.219; scale 1.209

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

221	18	15 16	13 14	11 12	10	တ ထ	7	თ თ	4	ω	N	1	Sult No.
	335	ა ა ა ა ა ა	35 35	35 35	35	u u u	35	3 <b>7</b>	37	37	37	37	Score
91.9 91.9 91.9			94.6 94.6	94.6 94.6				100.0 94.6		100.0	100.0	100.0	% Query Match
355 355 555	3411	880 922 3411	696 859	587 662	500	398 422	396	2105 389	692	384	208	115	% Query Match Length
	,		مار مار	$\mu$	ь,		<b>1-4</b>	<b></b>	ب	بر	Ь	μ	DB
YKB4_CAEEL RMAR_CANGA DVR1_BRARE RMAR_YEAST	POLG_YEFV2 YR7E_ECOLI	ARG2_YEAST CLPA_PEA POLG YEFV1	YHFK_ECOLI YQD3_CAEEL	DLD1_YEAST PMT7_YEAST	ANP1_YEAST	CHSY_ORYSA	CHSY_PINSY	POLR_ASGVP	YYI3_CAEEL	Y039_MYCPN	YFJJ_ECOLI	PTHY_HUMAN	ID
MITOCHONDRIAL RIBOSOMA DVR-1 PROTEIN PRECURSO MITOCHONDRIAL RIBOSOMA	ROTEIN (C	ARGININE METABOLISM RE ATP-DEPENDENT CLP PROT GENOME POLYPROTEIN (CO	HYPOTHETICAL 79.5 KD P HYPOTHETICAL 96.7 KD P	D-LACTATE DEHYDROGENAS DOLICHYL-PHOSPHATE-MAN	AMINONITROPHENYL PROPA	CHALCONE SYNTHASE (EC	SYNTHASE (EC	GENOME POLYPROTEIN (CN	•	HYPOTHETICAL PROTEIN M	HYPOTHETICAL 24.6 KD P	PARATHYROID HORMONE PR	· 5
3.44e+01 3.44e+01 3.44e+01 3.44e+01	ωμ		1.85e+01 1.85e+01	1.85e+01 1.85e+01	1.85e+01	1.85e+01	1.85e+01	5.14e+00 1.85e+01	ូច	5.14e+00	5.14e+00	5.14e+00	Pred. No.

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	Ц	_	بر	1	μ	μ	μ.	ب	μ	ш	ب	$\vdash$	щ	ш		ب	بر	ب	<b>j</b>	بر
YKQ0_CAEEL TOP2_CRIFA	EBN6_EBV	NIA_CICIN	VGLB_HCMVA	YOD3_CAEEL	SP02_MOUSE	RELA_STRCO	YER8_YEAST	HSF1_HUMAN	SKI_AVIES	YGCA_ECOLI	PO3B_XENLA	VANS_ENTFC	PO3A_XENLA	LEF3_NPVOP	YGCA_VIBSS	PTHY_BOVIN	Y080_BPP2	ZFH2_DROME	RYK_MOUSE	YCAJ_ECOLI
PUTATIVE ATP-DEPENDENT DNA TOPOISOMERASE II (	EBNA-6 NUCLEAR PROTEIN	NITRATE REDUCTASE (EC	GLYCOPROTEIN B PRECURS	HYPOTHETICAL 98.9 KD P	PRESYNAPTIC PROTEIN SA	GTP PYROPHOSPHOKINASE	HYPOTHETICAL 73.0 KD P	HEAT SHOCK FACTOR PROT	TRANSFORMING PROTEIN S	HYPOTHETICAL RNA METHY	TRANSCRIPTION FACTOR P	SENSOR PROTEIN VANS (E	TRANSCRIPTION FACTOR P	LATE EXPRESSION FACTOR	HYPOTHETICAL RNA METHY	PARATHYROID HORMONE PR	HYPOTHETICAL 8.3 KD PR	ZINC-FINGER PROTEIN 2	TYROSINE-PROTEIN KINAS	HYPOTHETICAL 49.6 KD P
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2 2	VASICEK T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J.,
P.	NATL: ACAD: SCI. U.S.A. 80:2127-2131(1983
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P. P.	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;
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2 2	MEDLINE: 74111656.
R.	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,
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R	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,
RE	(1975).
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MEDLINE; 75146516. KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.; BICCHEMISTRY 14:1842-1847(1975).

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X MEDLINE; 91009811.

A ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

L. J. CLIN. INVEST. 86:1084-1087(1990).

C. I. FUNCTION, PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

C. BONE AND PREVENTING THEIR RENAL EXCRETION.

C. I. SEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED

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MEDLINE; 7327467.
ANDREATTA R.H., HARTMANN A., JOEHL A.,
RINIKER B., RITTEL W., SIEBER P.;
HELV. CHIM. ACTA 56:470-473(1973).
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MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MPsrch_pp on : protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:27:11 1998; MasPar time 2.64 Seconds 52.320 Million cell upda

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Description: Perfect Score: Title: >US-08-817-547A-13 (1-9) from US08817547A.pep 62

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Scoring table: PAM 150 Gap 15 Sequence:

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match Listing first 45 summaries

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1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
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Statistics: Mean 15.334; Variance 52.987; scale 0.289

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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[Mys20]-hPPH(1-36)-NH [Morpholine-2-carboxy [Hexxhydropyridazine- N-Dimethyl-[Ala]-hPT [Hyp1]-hPTH(1-36)-NH2 Human paprthyroid hor Acetyl-hPTH(1-36)-NH2 [Lys(Isopropyl)]3]-hPT [Pyridine-2-carboxyli [D-val35]-hPTH(1-36)-GH [Mys3]-hPTH(1-36)-GH Human parathyroid hor Fusion protien compri Human parathyroid hor	R47971	R21243	R23245	R21251	R21250	R34460	R30851	R21152	R21153	W29420	R21199	R21198	W25687	W21946	P30015	R58164	R58295	R58175	R58242	R58246	o	R58247	R58248	R58176	817	827
	equence of a	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	Generic human parathy	parathyroid	parathyroid	parathyroid	parathyroid		Human parathyroid hor	Fusion protien compri	Human parathyroid hor	[Asp33]-hPTH(1-38)-OH	[D-Val35]-hPTH(1-36)-	[Pyridine-2-carboxyli	[Lys(Isopropyl)13]-hP	Acetyl-hPTH(1-36)-NH2	paprthyroid	]-hPTH(1-36)-	N-Dimethyl-[Ala1]-hPT	[Hexahydropyridazine-	[Morpholine-2-carboxy	36)-

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R58181 standard; peptide; 34 AA.
R58181;
R58181;
20-SEP-1994 (first entry)
[Thr33, Ala34]-hPTH(1-34)-NH2.
Human parathyroid hormone; hPTH; variant; an calcium; depletion; fixation; resorption; os hypoparathyroidism.
                                                                                                                                                                                                                                      12-JUL-1993; 014384.

15-JUL-1992; GB-015009

18-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-001673.

19-APR-1993; GB-008033.
                                                                                                                                (SANO ) SAN---
(BAUE/) BAUER W.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
(SANO ) SANDOZ TERFINDUNGEN VERW GES MBH.
"Thert R, Bauer W, Breckenridge R, Ca
                          New active para-thyroid hormone variants - used for treating or preventing osteopprosis etc.

Example 179; Page 43; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteopprosis) or to treat
 hypoparathyroidism.
Sequence 34 AA;
                                                                                                                           Albert R, Bauer W, B
Gombert F, Gram H, L
Waelchli R, Rainer A;
WPI; 94-018352/03.
                                                                                                                                                                                                                                                                                                                                                                    GB2269176-A.
02-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                              modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                 "in
                                                                                                                                                                                                                                                                                                                                                                                                 amide form"
                                                                                                                                                       Cardinaux F; P, Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analogue;
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RESULT
ID W1
AC W1
DT 25
DE H1
KW 08
KW 08
KW 08
FH K
OS K
OS H
FT m
Search completed: Thu Jul 30 10:27:26 1998 Job time: 15 secs.
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                                                                                                                 uery Match 100.0%;
est Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                    bone fracture

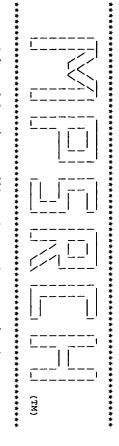
Claim 11; Page -; 33pp; English.

The present sequence is a specific example of a human parathyroid hormone (hpTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 is alpha-aminoisobutyric acid (Aib). In this example the Ser residue at position 3 of the wild-type has been substituted by Aib. The hpTH analogues stimulate bone growth and so are useful in human or veterinary conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).
                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1997.
30-JAN-1997.
30-JAN-1996; U11292.
30-JUL-1995; US-001105.
30-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
Dong ZX;
WPI; 97-118819/11.
New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and broad fracture.
                                                                                                                                                                         N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim.

Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UT 2
W17957; standard; peptide; 34 AA.
W17957;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Aib3]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture.
Bone fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9702834-A1.
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                                                              HNLGKHLNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
/note= "In amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label-
                                                                                                                 Score 62; DB 22;
Pred. No. 4.68e+00;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                   0;
                                                                                                                                             Length 34;
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm on: Thu Jul 30 10:26:25 1998; MasPar time 3.14 Seconds 104.605 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-817-547A-13 (1-9) from US08817547A.pep 62 1 HNLGKHLNS 9

Scoring table: PAM 150 Gap 15

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

120441 seqs, 36531193 residues

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.210; Variance 26.968; scale 0.787

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

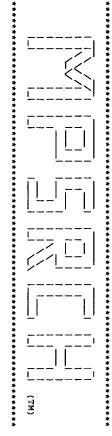
## SUMMARIES

23 23 24 44 45 46 47 47 47 47 47 47 47 47 47 47 47 47 47	sult No.
00000000000000000000000000000000000000	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 93.5 93.5 93.5 93.5 93.5 93.5 93.5 93.5	Query
34 34 34 35 35 35 35 37 37 37 37 37 37 37 37 37 37 37 37 37	Length
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	8
12WA 12WE 12WE 12WF 11WF 11WD 11WD 12WD 11WD 11WC 12WC 11WC 11WC 12WC 151851 15	IB
parathyroid hormone (parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 6 parathyroid hormone 6 parathyroid hormone 6 parathyroid hormone 9 parathyroid hormone 1 parathyroid hormone 1 parathyroid hormone 9 parathyroid hormone 1 parathyroid hormone 9	Description
4.02e-03 4.02e-03 4.02e-03 4.02e-03 4.02e-03 3.38e-02 3.38e-02 5.70e-03 5.70e-02 5.70e-02 5.70e-02 5.70e-02 5.70e-02 5.70e-02 5.70e-03 6.03e-04 6.03e-04 6.03e-04	Pred. No.

44 71.0 186 2 A46464 apolipoprotein A-I - 44 71.0 261 2 S31394 apolipoprotein A-I - 44 71.0 265 2 A4618 apolipoprotein A-I - 44 71.0 265 2 A4618 apolipoprotein A-I - 44 71.0 317 2 A49915 gutQ homolog - Escher 44 71.0 386 2 D42528 B23R protein - vaccim 44 71.0 386 2 D42528 ATP-binding protein - 44 71.0 1447 2 S63669 UDB9lucose - 91ycoprot 45 69.4 310 2 C47045 ferrochelatase (EC 4. 46 69.4 310 5 IFJI ferrochelatase (EC 4. 47 69.4 310 5 S59330 ATP-binding protein - 48 69.4 310 5 S59330 ATP-binding protein - 49 69.4 1021 2 S44644 Ferrochelatase (EC 4. 49 69.4 1021 2 S44644 F37A4.7 protein - Cae 49 69.4 2317 2 I56752 c-ros-1 unknown protein 49 69.4 2317 2 I56752 c-ros-1 tyrosine kina 40 69.4 2317 2 I56752 c-ros-1 tyrosine kina 41 69.4 2317 2 I56752 c-ros-1 tyrosine kina 42 67.7 193 2 R53835 hase-related protein 43 69.4 27 193 2 R54361 heat shock protein delated protein 44 67.7 4930 2 E69679 polyketide synthase p	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
186 2 A64464 site-specific colors of the col	42	42	42	42	43	43	43	43	43	43	43	43	43	44	44	44	44	44	44	44	44	40
2 A64464 2 A7915 2 A79704 2 A79704 3 A79715 2 A79716 2 A7	67.7	67.7	67.7	67.7	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	71.0	71.0	71.0	71.0					٠
A64646 site-specific J00704 apolipoproteir S31394 apolipoproteir A46018 apolipoproteir A46018 apolipoproteir A49915 Ba3R protein A49915 Ba3R protein A49916 Harbinding proteir A49916 Harbinding proteir A49916 Harbinding proteir A49916 Harbinding proteir A49917 Harbinding proteir A49918 Harbinding proteir A49918 Harbinding proteir A49918 Farrochelatase C47045 Farrochelatase C47045 Farrochelatase A53640 F37A4.7 proteir A53831 F37A4.7 proteir A53835 Farrochelatase S64361 Harbinding S64361 Harbindi	4930	417	292	193	2340	2338	2317	1854	1021	985	310	310	308	1447	585	386	317	265	264	231	186	ATO
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repectfic poprotein poprotein poprotein poprotein protein shock protein shock protein shock protein pr	E69679	S20608	S64361	A53835	148310	173957	I56752	I73956	S44644	S59330	1FJI	C47045	1AK1	S63669	G64220	D42528	A49915	A46018	S31394	JQ0704	A64646	504050
		heat shock protein Hs	hypothetical protein	protein	kinase-related prote1	tyrosine	tyrosine				_	Ö E C	ferrochelatase (EC 4.	UDPglucoseglycoprot	ATP-binding protein m	protein -	homolog -	ipoprotein		A-I		

RESULT 2 ENTRY TITLE TITLE ALTERNATE_NAMES HPPH(4-37) PDB_TITLE ORGANISM REFERENCE # authors # submission submitted to # cross-references PDB:1ZWE REFERENCE # authors # authors in Strukture # cross-references pDB:1ZWE REFERENCE # authors in Strukture # pp.0, Bayr	Query Match Best Local Similarity Matches 9; Conse: Db 9 HNLGKHLNS 17 Qy 1 HNLGKHLNS 9	KEYWORDS FEATURE 6-9 19-30 SUMMARY	ors	E Ors ission s-referen	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM
12WE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:12WE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	100.0%; Score 62; DB 5; Length 34; larity 100.0%; Pred. No. 4.02e-03; Conservative 0; Mismatches 0; Indels 0; Gaps 0; INS 17 II INS 17	hormone #region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629	Marx, U.C. Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR	Marx, U.C. the Brookhaven Protein Dat	TWA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures #formal name Homo sapiens #common name man

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COMMENT COMMENT Resolution: Note applicable COMMENT REAVORDS PATURE 15-25 #region helix (right hand alpha) SUMMARY #region helix (right hand alpha) #region helix (ri
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Psrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:25:15 1998; MasPar time 2.12 Seconds 106.609 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-13 (1-9) from US08817547A.pep 62 1 HNLGKHLNS 9

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.158; Variance 22.443; scale 0.987

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult	Score	Query Match	Length DB	Ü	ID	Description	Pred. No.
1	62	100.0	115	" ;	PTHY_HUMAN	PARATHYROID HORMONE PR	1.55e-04
N	58		115	H	PTHY_PIG	HORMONE	2.07e-03
ω	58	93.5	115	 -1	PTHY_CANFA	PARATHYROID HORMONE PR	2.07e-03
4	58	93.5	115	μ	PTHY_BOVIN	PARATHYROID HORMONE PR	
υ	57		115	4	PTHY_RAT	PARATHYROID HORMONE PR	3.90e-03
6	48	77.4	171	٠,	PAIA_BACSU	PROTEASE SYNTHASE AND	8.66e-01
7	47	75.8	621	۳	PLAK_MOUSE	JUNCTION PLAKOGLOBIN (1.52e+00
œ	47	75.8	738	μ	PLAK_XENLA	JUNCTION PLAKOGLOBIN (1.52e+00
9	47	75.8	743	ш	PLAK_HUMAN	JUNCTION PLAKOGLOBIN (1.52e+00
10	45	72.6	187	-	ATPD_ODOSI	ATP SYNTHASE DELTA CHA	4.57e+00
11	45	72.6	381	_	DHB2_MOUSE	ESTRADIOL 17 BETA-DEHY	4.57e+00
12	44	٠	265	-	APA1_PIG	APOLIPOPROTEIN A-I PRE	7.80e+00
13	44		317		KSF1_ECOLI	KPSF PROTEIN.	7.80e+00
14	44	71.0	386	_	VC17_VACCC	PROTEIN C17/B23.	7.80e+00
15	44	71.0	585	_	Y187_MYCGE	HYPOTHETICAL ABC TRANS	7.80e+00
16	43	69.4	310	-	HEMZ_BACSU	FERROCHELATASE (EC 4.9	1.32e+01
17	43	69.4	985	_	NAH_YEAST	PROBABLE NA(+)/H(+) AN	1.32e+01
18	43		1021	_	YPT7_CAEEL	HYPOTHETICAL 111.7 KD	1.32e+01
19	42	67.7	180	-	Y088_METJA	HYPOTHETICAL PROTEIN M	2.21e+01
20	42		192	۳	SC72_YEAST	TRANSLOCATION PROTEIN	2.21e+01
21	42	67.7	246	ш	SR1A_PHYPO	SPHERULIN 1A PRECURSOR	2.21e+01
22	42	67.7	292	ب	YG29_YEAST	HYPOTHETICAL 34.0 KD P	2.21e+01
23	42	67.7	417	1	HS47_HUMAN	47 KD HEAT SHOCK PROTE	2.21e+01

44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
40	40	41	41	41	41	41	41	41	41	41	41	41	41	42	42	42	42	42	42	42
64.5 64.5	64.5	66.1	66.1	66.1	66.1	66.1	66.1		66.1	66.1	66.1	66.1	66.1	67.7	67.7	67.7	67.7	67.7	67.7	67.7
614 2245	192	1444	750	592	527	522	405	382	300	279	270	245	105	1950	1184	887	505	418	417	417
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YQZ2_CAEEL MYSJ_DICDI	YOHD_ECOLI	RRPL_RDV	PSM_HUMAN	Y036_HAEIN	YD05_YEAST	SR54_SCHPO	HS47_CHICK	VATC_HUMAN	VA32_VACCV	REPJ_ECOLI	VA32_VARV	PFLA_ECOLI	YBXF_STAAU	UBR1_YEAST	BIMC_EMENI	MTS4_SCHPO	SMI1_YEAST	CBP2_HUMAN	HS47_MOUSE	HS47_RAT
MYOSIN IJ HEAVY CHAIN.	HYPOTHETICAL 21.4 KD P	RNA-DIRECTED RNA POLYM	PROSTATE-SPECIFIC MEMB	ABC	HYPOTHETICAL 60.9 KD P	SIGNAL RECOGNITION PAR	47 KD HEAT SHOCK PROTE	VACUOLAR ATP SYNTHASE	PROTEIN A32.	REGULATORY PROTEIN REP	PROTEIN A32.	PYRUVATE FORMATE-LYASE	PROBABLE RIBOSOMAL PRO	N-END-RECOGNIZING PROT	KINESIN-LIKE PROTEIN B	26S PROTEASOME REGULAT	SMI1 PROTEIN (KILLER T	COLLAGEN-BINDING PROTE	47 KD HEAT SHOCK PROTE	47 KD HEAT SHOCK PROTE
6.02e+01 6.02e+01	6.02e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01		3.67e+01	2.21e+01	2.21e+01	2.21e+01	2.21e+01	2.21e+01		2.21e+01

RESULT 1 ID PHIL HUMAN STANDARD; PRT; 115 AA. PC 01270; PO1270; PRT; 105 AA. PC 21_JUL-1996 (REL. 01, CREATED) OT 21_JUL-1996 (REL. 05, LAST SEQUENCE UPDATE) OT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE) OT 10-NOV-1997 (REL. 05, LAST SEQUENCE UPDATE) OT 10-NOV-1997 (REL. 05, LAST SEQUENCE UPDATE) OF PARATHYROLD HORMONE PRECURSOR (PARATHYRIN) (PTH). SHOWS SAPIENS (HUMAN). CEUTHERLA; PRIMATES. RP SEQUENCE FROM N.A. RA HENDLY GN., KRONENBERG H.M., POTTS J.T. JR., RICH A.; PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981). RR SEQUENCE FROM N.A. RA HENDLINE; 83169834. RA HENDLINE; 83169834. RA HENDLY GN., POTTS J.T. JR., RICH A., KRONENBERG H.M.; PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983). RA HENDLY GN., FOTTS J.T. JR., RICH A., KRONENBERG H.M.; RA HENDLY GN., KEMPER B., NIALL H.D., HABBENER J.F., POTTS J.T. JR.; RA JACOBS J.W., KEMPER B., NIALL H.D., HABBENER J.F., POTTS J.T. JR.; RA JACOBS J.W., KEMPER B., NIALL H.D., KEUTMANN H.T., SEGRE G.V., RA MEDLINE; 7411456. RA MATURE 249:155-157(1974). RA MEDLINE; 79082855. RA NIALL H.D., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H., RA NIALL H.D., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H., RA NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N., RA SEQUENCE OF 1-83 AND 84-115. RA KEUTMANN H.T., KABUER M.M., HENDY G.N., BARLING P.M., HENDY G.N., RA KEUTMANN H.T., KABUER M.M., HENDY G.N., BARLING P.M., HENDY G.N., RA CO'RIORDAN J.L.H., POTTS J.T., JACOBS J.W., BARLING P.M., HENDY G.N., RA CO'RIORDAN J.L.H., POTTS J.T., JACOBS J.W., BARLING P.M., HENDY G.N., RA CO'RIORDAN J.L.H., POTTS J.T., JACOBS J.W., BARLING P.M., HENDY G.N., RA CO'RIORDAN J.L.H., POTTS J.T., EXCERPTA MEDICA FOUNDATION, AMSTERDAM, RA L(1975).
<u> </u>

REVISIONS.
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
BIOCHEMISTRY 14:1842-1847(1975).

POTTS J.T. JR.;

SYNTHESIS OF 32-65.

```
RX MEDLINE; 91009811.

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

RA KRONENBERG H.M.;

RI J. CLIN. INVEST. 86:1084-1087(1990).

C1 - FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN PROBLEM TO PREVENTING THEIR RENAL EXCRETION.

C2 -- FORE AND PREVENTING THEIR RENAL EXCRETION.

C3 -- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED HYPOPARATHYROIDISM (FIH).

C4 -- HYPOPARATHYROIDISM (FIH).

C5 -- EMBL; JO0301; G190704; -.

C6 -- EMBL; JO0301; G190704; -.

C7 -- EMBL; JO0301; G190704; -.

C8 -- EMBL; JO0301; G190704; -.

C8 -- EMBL; JO0301; G190704; -.

C9 -- PIR; A01536; DTHU

C9 -- PIR; A19339; A19339.

C9 -- PIR; A19339; A19339; A19339.

C9 -- PIR; A19339; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
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Matches 9; Conservative
                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                   SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95318084
MARX U.C., AUSTERVANN S., BAYER P.,
STICHT H., WALTER S., SCHMID F.-X.,
ROESCH P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRÜCTURE BY NMR OF 32-65.
MEDLINE; 93345518.
MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNTHESIS OF 32-65.

MEDLINE; 73227467.

ANDREATTA R.H., HARTMANN A., JOEHL A.,

RINIKER B., RITTEL W., SIEBER P.;

HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT ARG-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 32-68
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                                                                                                                                                                                                                           PS00335; PARATHYROID; 1.
SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
                                                                                          107
115
                                                                                                                                                                                                                                                                                                                     16-JUN-97.
                                                                                              AA;
                                                                                            107
12861
                                                                                                                                                      25
31
115
18
                                                                                            WW;
        Score 62; DB 1; I
Pred. No. 1.55e-04;
0; Mismatches 0
                                                                                 PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEF)
PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
; 243E87C7 CRC32;
      Mismatches
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JAENICKE
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Gaps
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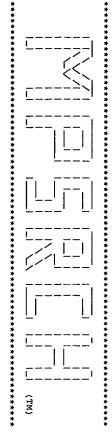
Search completed: Thu Jul Job time : 6 secs.

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Best Local S
Matches
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                                                                      PROPEP
CHAIN
SEQUENCE
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EUKARYOTA; METAZOA; CHOR
EUTHERIA; ARTIODACTYLA.
[1]
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 87316938.
SCHMELZER H.-J., GRO
NUCLEIC ACIDS RES. 1
                                                                                                                                     SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RI POTTS J.T. JR.;
BIOCHEMISTRY 13:1994-1999(1974).

1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; X05722; G1839; -.
                                                                                                 HORMONE; SIGNAL.
SIGNAL 1
                                                                                                                            EMBL;
PIR; A
PIR; B
                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986
01-JAN-1988
01-FEB-1996
                                                                                                                    PROSITE;
                                                                                                                                                                                               SEQUENCE OF 32-115. MEDLINE; 74253317.
                                                                                                                                                                                                                      MEDLINE; 76018954.
CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T.,
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                   SEQUENCE OF 26-115.
               40 HNLGKHLSS 48
                                                                                                                                                                                                                                                                                                                                                      PARATHYROID
                                                                                                                                                                                                                                                                                                                                                                                                PTHY_PIG
 سا
                                                                                                              ; A01535; PTPG.
; B26806; B26806.
;SITE; PS00335; PA
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HNLGKHLNS
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                                            Similarity
                                                                     1
26
32
115 AA;
                                 93.5%;
llarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                              (REL. 01, CREATED)
(REL. 06, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
9
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S. 15:6740-6740(1987).
                                                                                                                 PARATHYROID;
                                                                    25
31
115
12852
                                                                                                                                                                                                                                                                                                                     CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                      WW.
                               Score 58; D. Pred. No. 2.
                                                                  PARATHYROID HORMONE.
; 98B67F47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                Mismatches
                             DB 1; LC., 2.07e-03; 0;
                                                                                                                                                                                                                                                                                                                                                                                               115 AA
                                                                                                                                                                                                                                                                            MAYER
                                                                                                                                                                                                                              HAMILTON J.W., COHN D.V.;
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                                                Length 115;
                              Indels
                                                                                                                                                                                 O'RIORDAN J.L.H.,
                                                                                                                                                         THE SALTS
                              0;
                             Gaps
                             0
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srch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:25:38 1998; MasPar time 3.77 Seconds 100.539 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-13 (1-9) from US08817547A.pep 62 1 HNLGKHLNS 9

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.246; Variance 22.169; scale 0.958

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Reg
20 20 20 20 20 20 20 20 20 20 20 20 20 2	Result
ν 7 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 6	Score
771.000.0000.00000000000000000000000000	Query Match Length
105 421 172 172 174 745 568 385 385 385 385 387 387 181 301 301 301 301 327 227 227 298	Length
110 110 110 110 110 110 110 110 110 110	BIG
0283473 028532 032112 015093 015093 015093 0150565 674405 674405 0182730 01827	IB
PARATHYROID HORMONE (F HYPOTHETICAL 48.5 KD P TRANSCRIPTIONAL REGULA PLAKOGLOBIN (FRAGMENT) PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. HYPOTHETICAL 62.3 KD P 17-BETA HYDROXYSTEROID HUNCHBACK GAP (FRAGMEN CHROMOSOME XV READING COSMID F31D5. APOLIPOPROTEIN A-I (FR VPR PROTEIN. SITE-SPECIFIC RECOMBIN KYPR PROTEIN. SITE-SPECIFIC RECOMBIN KYPR GENE. UDP-GLC:GLYCOPROTEIN UDP-GLC:GLYCOPROTEIN UDP-GLC:GLYCOPROTEIN WNT-LIKE PROTEIN WNT14 BASIC TRANSCRIPTION FA	Description
6.194-03 6.196-01 1.996-00 1.926-00 1.926-00 1.926-00 1.926-00 1.926-00 5.796-00 5.796-00 5.796-00 9.926-00 9.926-00 9.926-00 9.926-00 9.926-00 9.926-00 9.926-00 9.926-00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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66.1	٠	66.1	•	66.1				66.1	66.1	67.7	67.7	67.7	67.7	67.7	67.7	67.7	67.7	69.4	69.4	69.4	69.4	69.4	69.4	69.4
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Q12923	Q28006	Q15265	Q50177	013705	006585	Q22494	Q90420	Q63778	Q89195	031783	P93820	028232	P77814	Q84584	021973	Q55024	P88152	Q60705	Q64736	Q63132	Q63130	Q63131	001906	Q22312
PROTEIN TYROSINE PHOSP	BA14 TYROSINE PHOSPHAT	PROTEIN TYROSINE PHOSP	PROBABLE CYCLIC SYNTHE	HYPOTHETICAL 95.0 KD P	HYPOTHETICAL 53.5 KD P	TOS. CEREV	47 KDA HEAT SHOCK PROT	HYPOTHETICAL 43.7 KD P	VACCINA VIRUS GENOMIC	POLYKETIDE SYNTHASE OF	HYPOTHETICAL 110.0 KD	HTNY	PROLIDASE (EC 3.4.13.9	EQUE	HYPOTHETICAL 31.3 KD P	NUTRIENT-STRESS INDUCE	VPR PROTEIN.	ROS1 PROTOONCOGENE (PR	ROS1 PROTOONCOGENE (C-	RAT HEART-DERIVED C-RO	RAT LUNG-DERIVED C-ROS	RAT LUNG-DERIVED LO1 C	COSMID F59E12.	COSMID TO7E3.
	4.74e+01	4.74e+01	4.74e+01	4.74e+01	4.74e+01	٠	4.74e+01	٠	4.74e+01	•		•	2.84e+01		2.84e+01	2.84e+01	2.84e+01	1.69e+01	1.69e+01	:	1.69e+01	:	1.69e+01	1.69e+0

DT 01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE) D1 01-JAN-1998 (TREMBLEL 05, LAST ANNOTATION UPDATE) D2 PARATHYROID HORMONE (FRAGMENT). GN PTH. GN PTH. GN PTH. GN PTH. OC EUGRAYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; CLUTHERIA; RODENTIA. RN [1] RP SEQUENCE FROM N.A. RC TISSUE-THYROID, AND PARATHYROID; RA SCHMELZER H.J., GROSS G., MAYER H.; RL ADV. GENE TECHNOL. 21:228-229(1984). DR EMBL; M54875; G601933; FT NON_TER 1 1 1 1 SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32; PT NON_TER 2 SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32; Query Match Best Local Similarity 88.9%; Pred. No. 4.94e-03; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps D5 30 HNLGKHLAS 38 D6 31 HNLGKHLAS 38 D7 11
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RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., RA REICH C.I., MCMEELL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R., RA GOCAYNE J.D., WEIDMAN J.E., MCDONALD L., CUTTERBACK T., COTTON M.D., RA GOCAYNE J.D., WEIDMAN J.E., MCDONALD L., CUTTERBACK T., COTTON M.D., RA GOCAYNE J.D., WEIDMAN J.E., MCDONALD L., CUTTERBACK T., COTTON M.D., RA GOCAYNE J.D., WEIDMAN J.E., MCDONALD L., CUTTERBACK T., COTTON M.D., RA GOLSEN G.J., FRASER C.M., SANTH H.O., WOESE C.R., VENTER J.C.; RA GOLSEN G.J., FRASER C.M., SANTH H.O., WOESE C.R., VENTER J.C.; REICHGE FROM N.A.

RA SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

RI SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

RA DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., AND DOSON R.J., KORNANG T.M., BADGER E.K., PETERSON J.D., RICHARDSON D.L., CHARLES E.F., RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCMEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R., RA GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D., SUBMITTED (NOV1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

PA CLISH C.I., MCHELL L.K., BADGER J.H., SYKES S.M., SADOW P.W., CONSEN G.J., FRASER C.M., SANTH H.O., WOESE C.R., VENTER J.C.; BEML; AED00982; G2548811; ".

PA CLISH G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; BEML; AED00982; G2548811; ".

QUETY MATCH PROTEIN.

SO SEQUENCE 421 AA; 48473 MM; D1467826 CRC32;

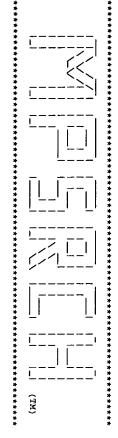
QUETY MATCH PROTEIN.

SO SEQUENCE THAN JUL 30 10:26:08 1998

Search completed: Thu Jul 30 10:26:08 1998

Search completed: Thu Jul 30 10:26:08 1998

Search completed: Thu Jul 30 10:26:08 1998
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NPSTCh_pp protein - protein database search, using Smith-Waterman algorithm on:

n on: Thu Jul 30 10:29:27 1998; MasPar time 2.68 Seconds 45.741 Million cell updates/sec Tabular output not generated.

Title: >US-08-817-547A-14
Description: (1-8) from US08817547A.pep
Perfect Score: 58
Sequence: 1 HNLGKHLN 8

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.991; Variance 49.457; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 3 3 3 4 4 4 7 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
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111111111111111111111111111111111111111	Query Match
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R58241 W17949 W17958 W17955 W17969 W17969 W17969 W17969 W17969 W179622 W17943 W17943 W17943 W17948 R74514 R74514 R74514 R74506 R74431 R58088	IJ
[N1e8,18,D-Asn33,D-Ph Human parathyroid hor Human parathyroid of Human parathyroid hor Human parathyroid hor Thuman parathyroid hor Human parathyroid hor Human parathyroid hor Parathyroid hormone p	Description
7.41e+00 7.41e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	5 8	58	ŭ
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115 :	84	84											38												
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R75693	R21243	R23245	R21251	R21250	R34460	R30851	W29420	W25687	W21946	P30015	R58162	R58166	R58134	R58122	R58121	R58163	R58282	R24778	R23995	R58263	R58214	R58213	9	R58281	2
_	Ω			parathyroid		Generic human parathy		Human parathyroid hor	Fusion protien compri	parathyr	-hPTH(1-38)]-hPTH(1-38)	-hPTH(1-38)-	1-38)	-38	[Pro33]-hPTH(1-38)-OH	[Trp(SO2Pmc)23]-hPTH(hPTH(1-37)-amide/ethy		[D-Ile5]-hPTH(1-36)-N	[Ala19]-hPTH(1-36)-NH	(1-36)	ln18]-hPT	[D-Val21]-hPTH(1-36)-	[D-G1u4]-hPTH(1-36)-N
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Example 239; Page 45; 92pp; English. This peptide is an example of a highly generic formula covering	8352/03. para-thyroid	7	Bauer W, Breckenridge R, Cardinaux F;	(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.	/) BAUER 1	o١	1003;	28-JAN-1993; GB-001692.	28-JAN-1993; GB-001691.			GB.	•••	12-JUL-1993; 014384.	2-FEB-19			1				miso difference 33					Synthetic.	•	n; resorption;	Human parathyroid hormone; hPTH; variant; analogue;	[N1e8, 18, D-Asn33, D-Phe34]-hPTH(1-34)NH2.	20-SEP-1994 (first entry)	PABANI.	700/1 standard. postido. 3/

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSS PRAGE TO STANDARD 
                                                                                                                                                                                                                                          Claim 7; Page -; 33pp; English.

The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one cof the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 cc is cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). The hPTH analogues stimulate consistion 24 and 28, and the val residue at position 31 of the cyclohexylalanine substituted by Cha. The hPTH analogues stimulate consumer to steeporosis and bone fracture, optionally in conjunction creatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).

CL N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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03-JUL-1996; U1292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dong 2X; wp1; 97-118819/11.

New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W17949;
29-UUL-1997 (first entry)
Human parathyroid hormone analogue [Cha24,28,31]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone fracture
Claim 7; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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28
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'note = "Cha"
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                                                                                                                 Score 58; DB 22; L
Pred. No. 7,41e+00;
0; Mismatches 0;
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Pred. No. 7.41e+00;
0; Mismatches 0
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Search completed: Thu Jul 30 10:29:43 1998

Job time : 16 secs.

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***********************	(FM)	*******************

MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:28:51 1998; MasPar time 3.31 Seconds 88.370 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-14 (1-8) from US08817547A.pep 58 1 HNLGKHLN 8

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.760; Variance 25.957; scale 0.800

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 2 2 3 3 3 3 4 4 4 4 4 7 7 7 7 112 113 114 115 116 117 117 118 119 119 119 119 119 119 119 119 119	sult No.
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Score
100.0 100.0	Query Match
34 34 34 34 35 35 37 37 37 37 37 37 37 37 37 37 37 37 37	Length
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12WA 12WG 12WG 12WG 12WG 12WG 12WG 11ZWD 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 11HTH 1 H 1	ID
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41	41	41	41	41	41	42	42	42	42	42	42	42	43	43	43	43	43	43	43	43	4
70.7	70.7	70.7	70.7	70.7	70.7	72.4	72.4	72.4	72.4	72.4	72.4	72.4	74.1	74.1	74.1	74.1	74.1	74.1		74.1	
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A43377	S77657	D64044	S21976	A40968	S20608	E69679	S12332	S63669	F69505	S64361	B29624	H64310	S44644	A32905	S35093	S35092	S54636	C47045	1FJI	1AK1	001660
RNA-directed RNA poly	cyclic peptide synthe	hypothetical protein	probable RNA-directed	heat shock protein 47	protein	polyketide synthase p	ubiquitinprotein li	UDPglucoseglycoprot	m			hypothetical protein	F37A4.7 protein - Cae	plakoglobin, desmosom	plakoglobin – African	plakoglobin – mouse (	probable membrane pro	ferrochelatase (EC 4.	ferrochelatase (EC 4.	ferrochelatase (EC 4.	THE PARTY PARTY AND THE PARTY
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RESULT 2  ENTRY  TITLE  ALTERNATE NAMES HPTH(4-3-7)  PDB_TITLE  Structure of  Structures  ORGANISM REFERENCE  #authors #submission #cross-references PDB:1ZWE  REFERENCE  REFERENCE  #authors #submission #cross-references PDB:1ZWE  REFERENCE  TN001721  #authors in Strukture pp.0, Bayr	Query Match Best Local Simil Matches 8; Db 9 HNLGKHLN                     Qy 1 HNLGKHLN	KEYWORDS FEATURE 6-9 19-30 SUMMARY	k hors	ORGANISM #to: REFERENCE A67/ #authors Roes #submilssion submilssion submilssio	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
1ZWE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 Rossch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 roes PDB:1ZWE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	1 100.0%; Score 58; DB 5; Length 34; Similarity 100.0%; Pred. No. 1.85e-02; 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; GKHLN 16	hormone  #region helix (right hand alpha)\ #region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629	TR001717  Marx, U.C.  in Strukturen Verschiedener Parathormonfragmente in Loesung,  pp.0, Bayreuth : University of Bayreuth (Thesis), 1996  Resolution: not applicable  Defermination: NAME	#format_name Homo sapiens #common_name man A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:1ZWA	77.4

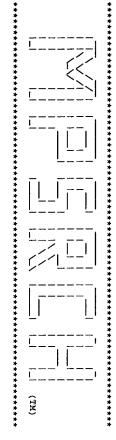
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COMMENT Determination: NNR
COMMENT Determination: NNR
KEYWORDS
FEATURE
15-25

#region helix (right hand alpha)
SUMMARY
Atch
100.0%; Score 56: DB 5: Length 34;
Best Local Similarity 100.0%; Pred. No. 185e-02;
Matches B: Conservative O; Mismatches O; Indels O; Gaps O;

Db 6 HNLGKHLN 13
[11111]
Qy 1 HNLGKHLN B

Search completed: Thu Jul 30 10:29:09 1998

Job time: 18 secs.
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:27:45 1998; MasPar time 2.10 Seconds 95.669 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-14 (1-8) from US08817547A.pep 58 1 HNLGKHLN 8

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.688; Variance 21.433; scale 1.012

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

NO.	Score 58	70   GH	Length DB 115 1 115 1	<b>→</b>	ID PTHY_HUMAN	Description
ω N F	5 5 5	93.1	115			PARATHYROID PARATHYROID
л 4-	л U1 3 4	93.1	115	ــر د	PTHY_BOVIN	
<b>თ</b> (	48		171	٠,	PAIA_BACSU	
9 7	4 4 5	77.6 75.0	381		DHB2_MOUSE	
ம	44		386	<b></b> +	VC17_VACCC	
10	44		585	Н	Y187_MYCGE	
11	43	74.1	310	1	HEMZ_BACSU	
12	43	74.1	621	Н	PLAK_MOUSE	
13	43	74.1	738	1	PLAK_XENLA	JUNCTION
1 1 5	գ Ծ Ա	74.1 74.1	743 1021		PLAK_HUMAN	
16	42	72.4	180	Н	Y088_METJA	
17	42	72.4	246	Н	SR1A_PHYPO	
1 E	4 4 2 2	72.4	292 887	<b>-</b> -	MTS4_SCHPO	
220	42	72.4	1950		UBR1_YEAST	
22	41 41	70.7 70.7	187 245		ATPD_ODOSI	

45	44	43	42	41	40	39	38	37	36	ა წ	34	33	32	ω L	30	29	28	27	26	25	24
40	40	40	40	40	40	40	40	40	40	40	40	40	40	41	41	41	41	41	41	41	41
69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7
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FA5_HUMAN	GP21_RAT	MSH1_YEAST	YSPL_CAEEL	CPT1_RAT	YQZ2_CAEEL	Y187_MYCPN	ST13_SCHPO	Y240_MYCGE	Y240_MYCPN	VIF_HV2D1	YOHD_ECOLI	VPR_HV1N5	CPT1_MOUSE	RRPL_RDV	NAH_YEAST	Y036_HAEIN	CBP2_HUMAN	HS47_HUMAN	HS47_RAT	HS47_MOUSE	HS47_CHICK
COAGULATION FACTOR V P	INTEGRAL MEMBRANE GLYC	MUTS PROTEIN HOMOLOG 1	HYPOTHETICAL 91.0 KD P	MITOCHONDRIAL CARNITIN	HYPOTHETICAL 69.0 KD P	HYPOTHETICAL ABC TRANS	PUTATIVE ATP-DEPENDENT	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	VIRION INFECTIVITY FAC	HYPOTHETICAL 21.4 KD P	VPR PROTEIN (R ORF PRO	MITOCHONDRIAL CARNITIN	RNA-DIRECTED RNA POLYM	PROBABLE NA(+)/H(+) AN	HYPOTHETICAL ABC TRANS	COLLAGEN-BINDING PROTE	47 KD HEAT SHOCK PROTE			
3.85e+01					3.85e+01	3.85e+01		3.85e+01		3.85e+01	3.85e+01	3.85e+01	3.85e+01	2.30e+01	2.30e+01	2.30e+01	2.30e+01	2.30e+01	2.30e+01	•	2.30e+01

REFERE	RA	R P R	2 2 2	2 P 2	2 2 2	RA S	RP PP	R Z	P. R.	광 주	RN	RL	RA A	RX	RN	R.	R R	RP	8	88	S S	DE	ם ב	ğ	A E	RESULT
O'RICKDAN J.L.H., POTTS J.T., JK.; (IN) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975). [7]	O. ALL H.D., J.	FOITS J.I. JR.; BIOCHEMISTRY 17:5723-5729(1978).			O'RIOKDAN J.L.H., AOKBACH G.D., FOTTS J.T. JK.; PROC. NATI. ACAD. SCI. U.S.A. 71:384-388(1974). [8]	R.T., JACOBS J	SEQUENCE OF 32-68.			MEDLINE; 74174967.	[3]	NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983	VIII.	83169834.		NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).	MEDLINE; 82150870. HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.:		HERIA; PRIMATES.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	CADIENC (UITAAN)	HORMONE PR	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)	1986 (REL. 01, CREATED)	PO1270;	

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                CONFLICT
SEQUENCE
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SYNTHESIS OF
                                                                       SIGNAL
PROPEP
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MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
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MARX U.C., AUSTERWANN S., BAYER P., ADERMANN STICHT H., WALTER S., SCHMID F.-X., JAENICKE ROESCH P.;
                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                             ANDREATTA R.H., HARTMANN A., JOEHL A., RINIKER B., RITTEL W., SIEBER P.; HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.

KEUTWANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS

HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE; 75146516.
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
BIOCHEMISTRY 14:1842-1847(1975).
                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF MEDLINE; 95318084.
                                                        VARIANT
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                                                                                     PS00335; PARATHYROID; 1. SIGNAL; DISEASE MUTATION;
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                              PARATHYROID HORMONE.
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PROCESSING OF THE PRECU
N -> D (IN REF. 5).
W; 243E87C7 CRC32;
       Score 58; DB 1;
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FORSSMANN W.-G.,
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OC EUTHERIA;

RN [1]

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RA SCHEMELZER

RA SCHEMELZER

RA CHUCLEIC AC

RN [2]

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RX MEDLINE;

RA SCHEMIS;

RN [3]

RP SEQUENCE (
RX MEDLINE;

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RA SCHEMIS;

RN MEDLINE;

RA SAUER R.T

RA POTTS J.T

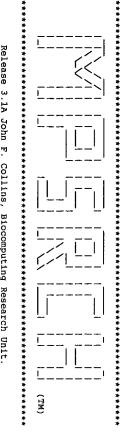
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01-JAN-1988
01-FEB-1996
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1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; X05722; G1839; -.
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MEDLINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 87316938. SCHMELZER H.-J., G
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SUS SCROFA (PIG).
EUKARYOTA; METAZOA;
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Similarity 87.5%;
7; Conservative
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(REL. 06, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
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S. 15:6740-6740(1987).
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12852
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                        10:27:51
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Pred. No. 1.17e-02;
1; Mismatches C
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MPsrch_pp 800 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:28:08 1998; MasPar time 3.81 Seconds 88.534 Million cell updates/sec

Tabular output not generated

Title: >US-08-817-547A-14 (1-8) from US08817547A.pep 58 1 HNLGKHLN 8

Sequence: Description: Perfect Score:

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb15

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

Statistics: Mean 20.802; Variance 21.214; scale 0.981

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

Result No.	Score	% Query Match	Length	DB	Ħ	Description	Pred. No.
1	53	91.4	105	10	Q63473	PARATHYROID HORMONE (F	2.85e-02
N	48	82.8	172	ဖ	032112	TRANSCRIPTIONAL REGULA	5.95e-01
ω	45	77.6	381	10	Q62730	17-BETA HYDROXYSTEROID	3.37e+00
4	45	77.6	421	و	028532	HYPOTHETICAL 48.5 KD P	3.37e+00
տ	45	77.6	1817	ω	Q19931	COSMID F31D5.	3.37e+00
თ	44	75.9	82	4	Q29248	APOLIPOPROTEIN A-I (FR	5.90e+00
7	44	75.9	96	11	Q72500	VPR PROTEIN.	5.90e+00
œ	44	75.9	301	1	Q70212	ENVELOPE GLYCOPROTEIN,	5.90e+00
9	44	75.9	568	ø	P74405	HYPOTHETICAL 62.3 KD P	5.90e+00
10	43	74.1	123	N	014904	WNT-LIKE PROTEIN WNT14	1.02e+01
11	43	74.1	171	N	Q15093	PLAKOGLOBIN (FRAGMENT)	1.02e+01
12	43	74.1	312	ω	Q22312	COSMID T07E3.	1.02e+01
13	43	74.1	414	w	001906	COSMID F59E12.	1.02e+01
14	43	74.1	619	ᆫ	Q99234	CHROMOSOME XV READING	1.02e+01
15	43	74.1	745	N	Q15151	PLAKOGLOBIN.	1.02e+01
16	43	74.1	745	10	P70565	PLAKOGLOBIN.	1.02e+01
17	43	74.1	2272	N	015020	KIAA0302 (FRAGMENT).	1.02e+01
18	42	72.4	96	11	P88152	VPR PROTEIN.	1.76e+01
19	42	72.4	283	7	021973	HYPOTHETICAL 31.3 KD P	1.76e+01
20	42	72.4	314	11	Q84584	GENOME, PARTIAL SEQUEN	1.76e+01

45	44	43	42	41	40	39	3 8	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	17
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69.0	69.0	69.0	69.0	69.0	69.0	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	72.4	72.4	72.4	12.4
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000578	035288	P77814	Q15430	025653	037116	Q13535	Q98631	Q50177	P97692	P78585	013705	000061	Q63289	006585	Q90420	018326	Q63778	013669	Q55024	Q29179	031783	Q09140	P93820	028232
KIAA0167.	CARNITINE PALMITOYLTRA	PROLIDASE (EC 3.4.13.9	COAGULATION FACTOR V (	SITE-SPECIFIC RECOMBIN	ENVELOPE GLYCOPROTEIN	FRAP-RELATED PROTEIN (	RNA-DEPENDENT RNA POLY	PROBABLE CYCLIC SYNTHE	L1 RETROTRANSPOSON ORF	PHOSPHOINOSITIDE-SPECI	HYPOTHETICAL 95.0 KD P	CYTOCHROME P-450 MONOO	L1 RETROPOSON, ORF2 MR	HYPOTHETICAL 53.5 KD P	47 KDA HEAT SHOCK PROT	HUNCHBACK GAP (FRAGMEN	HYPOTHETICAL 43.7 KD P	BASIC TRANSCRIPTION FA	NUTRIENT-STRESS INDUCE	CARNITHINE PALMITOYLTR	POLYKETIDE SYNTHASE OF	UDP-GLC:GLYCOPROTEIN G	HYPOTHETICAL 110.0 KD	THIMIDIDATE SINIHASE,
5.05e+01	5.05e+01	5.05e+01	5.05e+01	5.05e+01	5.05e+01			3.00e+01	3.00e+01	3.00e+01	3.00e+01			3.00e+01	1.76e+01	1.76e+01	1.76e+01	1./06+01						

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TISSUE-THYROID, AND PARATHYROID;
TISSUE-THYROID, GROSS G., MAYER H.;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.

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SEQUENCE 105 AA; 11746 MW; 6AC3163
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Q1-NOV-1996
Q1-JAN-1998
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22112 PRELIMINARY; PRT; 172 AA.
032112;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR.
STRAIN-168;
KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
                                                                                                                                                                                                                    BACILLUS SUBTILIS
                                                                                                                                                                                                                                                         PAIA.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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                                                                                                           SEQUENCE FROM N.A.
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1 HNLGKHL 7
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Local Similarity 100.0%;
hes 7; Conservative
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                                                                                                                                                                                      ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
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Pred. No. 2.85e-02;
0; Mismatches 0;
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                                                                                                                                          Query Match 82.8%; Score 48; DB 9; Length 172; B5.7%; Pred. No. 5.95e-01; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-168;

KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

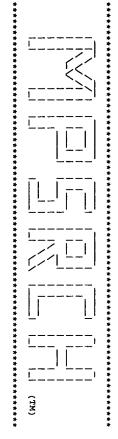
KUNST TEL, OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; 299120; E1164294;

EMBL; 299120; E1784294;

SEQUENCE 172 AA; 20015 MW; 2AA7F8CE CRC32;
                                                                                                                 105 HGLGKHL 111
                                                                                          1 HNLGKHL 7
                                                                                                                                            0,
                                                                                                                                     Gaps
                                                                                                                                     0,
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

In on: Thu Jul 30 10:31:15 1998; MasPar time 2.62 Seconds 40.993 Million cell updates/sec Tabular output not generated.

Title: >US-08-817-547A-15
Description: (1-7) from US08817547A.pep
Perfect Score: 53

Sequence: 1 HNLGKHL 7

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part5 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.515; Variance 42.487; scale 0.342

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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20000000000000000000000000000000000000	Length I
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RR22064 RR22064 RR53673 RF3415882 RF341576 RF341576 RF342576 RF342576 RF74444 RF7444 RF744 RF7444 RF744	Ħ
Modified hPTH(7-34)NH Accelerator peptide b Human parathyroid hor Cyclic parathyroid hormone/p Parathyroid hormone/p Parathyroid hormone/p Parathyroid hormone/p [Arg16,17]hPTH (1-34)NH2 [Lys16]hPTH (1-34)NH2 [Lys16]hPTH (1-34)NH2 Human parathyroid hor Human parathyroid hormone p Parath	Description
9.011ee	Pred. No.

Query Match 100.0%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 53; DB 4; Length 28; Pred. No. 9.01e+00; 0; Mismatches 0; Indels

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Gaps

0

45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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P40209	R23452	R21212	R23472	R21176	R23318	R23519	R34453	R34452	R23261	R21195	R23356	R23402	R21215	R34458	R23293	W25687	R30859	P30015	R98958	P20248	R58151	R58152	R58156	81	822
Sequence of prepropar	Porcine parathyroid h	Human parathyroid hor	Porcine parathyroid h	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho				Human parathyroid ho			Human parathyroid h	Leu8 hPTH (7-84) mute	Human parathyro		סי	_	[Arg22]	•	[Pro3,Thr33]-hPTH(1-3	[N1e8,18,27]-hPTH(1-3
9.01e+00	9.01e+00	•	9.01e+00		•		•			9.01e+00			٠	•	•	•	9.01e+00	9.01e+00		9.01e+00		•	9.01e+00	•	<u>`</u>

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osteoporosis and hyperparathyroidism.

Claim 1; Column 10; 6pp; English.

The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N,N-diisobutyl or 3-phenylpropanoyl. The PTH analogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bloactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bloassays to measure naturally occurring PTH and to diagnose the etiology of or to treat hyperthyroidism and diseases caused by abberrent produ. of hormone-like substances, such as tumours. It may also be used to treat immune diseases such as inflammation. It is prepd. by solid
                                                                                                                                                                                                                                                         New parathyroid hormone analogues - useful for treatment and vitro diagnosis of PTH-dependent tumours, immune disorders,
                                                                                                                                                                                                                                                                                                                                       US5093233-A.
03-MAR-1992.
25-APR-1990; 514394.
25-APR-1990; US-514394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified hPTH(7-34)NH2.
Parathyroid hormone; analogue; osteoporosis; hyperthyroidism; tumours; hypercalcaemia; renal failure; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R22064 standard; Protein; R22064;
               phase synthesis.
See also R22058-75.
                                                                                                                                                                                                                                                                                          WPI; 92-096233/12.
                                                                                                                                                                                                                                                                                                         (MERI ) MERCK & CO INC. Rosenblatt M, Roubini E,
                                                                                                                                                                                                                                                                                                                                                                                                                       modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        /label- NH2
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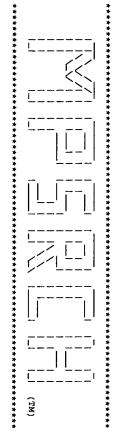
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RESULT
ID RE
AC RE
Search completed: Thu Jul 30 10:31:31 1998 Job time: 16 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID R62432 standard; peptide; 34 AA.

AC R62432;
DT 31-UUL-1995 (first entry)
DE Accelerator peptide basic region peptide, p-8.

KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW periodontal tissue; regeneration; periodontitis; periodontal pocket;
OS Synthetic.
PN J05234653-A.
PD 23-AUG-1994.
PP 10-FEB-1993; U4-5998.
PP 10-FEB-1993; U7-045998.
PP 10-FEB-1993; U7-045998.
PP 10-FEB-1993; U7-045998.
PP 10-FEB-1993; U7-045998.
CSUNZ ) SUNSTAR CLEM IND CO LTD.

WRI; 95-187631/21.
Accelerator for regenerating periodontal tissue - comprises periodontal periodontal tissue comprises plactosure; Page 3: 7pp; Japanese.
CC The sequences in R62425-36 are peptide fragments of an accelerator CC accelerator in R62425-36 are peptide fragments of an accelerator CC accelerator is applied by opening the gingiva, treating the tissue regeneration. The accelerator is applied by opening the gingiva, treating the tissue cCC destroyed by periodontal tissue regeneration. The accelerator is applied by opening the gingiva, treating the tissue cCC periodontal pocket. The accelerator reduces the down growth of the sequence 34 AA;

Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                            Score 53; DB 26; Length 34;
Pred. No. 9.01e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                   0;
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:30:52 1998; MasPar time 4.09 Seconds 62.524 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-15 (1-7) from US08817547A.pep 53 1 HNLGKHL 7

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.217; Variance 24.497; scale 0.825

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

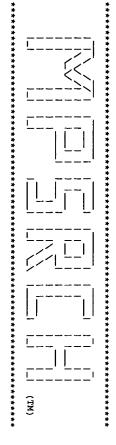
SUMMARIES

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40	40	40	40	40	40	40	40	40	40	40	41	41	41	41	41	41	41	41	41	42	42
75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	77.4	77.4		77.4		77.4	77.4	77.4	77.4	79.2	79.2
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S63669	A43377	S77657	A46627	S21976	E69467	E64226	S73826	D35119	H64310	S58066	E69679	S76244	I52968	S20608	A40968	A42843	A41252	D42528	S01789	S54636	F69505
UDPglucoseglycoprot	RNA-directed RNA poly	cyclic peptide synthe	carnitine palmitoyltr	probable RNA-directed		hypothetical protein	MG240 homolog F10_orf	protocatechuate 3,4-d	hypothetical protein	probable olfactory re	polyketide synthase p	hypothetical protein	colligin-2 - human	heat shock protein Hs	heat shock protein 47	heat shock protein Hs	heat shock protein 47	B23R protein - vaccin	pyruvate formate-lyas	probable membrane pro	thymidylate synthase
7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	3.07e+01	3.07e+01

#authors Roesch, P.; #submission submitted to #cross references PDB:12WF REFERENCE TN003318 #authors Marx, U.C. #book in Strukture	RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM	Matches 7;  Matches 7;  Db 6 HNLGKHL            1 HNLGKHL	Matc	R	REFERENCE TOOL	RESULT 1 ENTRY TITLE ALTERNATE_NAMES
ROUSCH, P.; Marx, U.C. ROUSCH, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 noes ppB:12WF TN003318 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung,	1ZWF #type complete parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures #formal_name synthetic ns770	Conservative 0; Misma 12	#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508 #length 34, Score 53; DB 5; Length 34; Gimilarity 100.0%; Score 53; DB 5; Length 34;	Marx, U.C.  Marx, U.C.  In Strukturen Verschiedener Parathormonfragmente in Loesung, in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth ; University of Bayreuth (Thesis), 1996  Resolution: not applicable  Determination: NMR  disease mutation; hormone; signal	#formal_name synthetic #67743 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:12WG TN003319	utant N-TERMINAL SUCCIN

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COMMENT
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RESOlution: not applicable
REMYORDS
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Psrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:30:01 1998; MasPar time 2.13 Seconds 82.367 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-15 (1-7) from US08817547A.pep 53 1 HNLGKHL 7

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.123; Variance 20.163; scale 1.048

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score   Match Length DB   ID   Description   Pred. No.	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	&	7	თ	տ	4	ω	2	1	NO.	sult
Length DB ID  Description  Pred. N  115 1 PTHY_BOVIN PARATHYROID HORMONE PR 8.04e- 115 1 PTHY_CANFA PARATHYROID HORMONE PR 8.04e- 115 1 PTHY_PIG PARATHYROID HORMONE PR 8.04e- 115 1 PTHY_HUMAN PTHY PIG PARATHYROID HORMONE PR 8.04e- 115 1 PTHY_HUMAN PARATHYROID HORMONE PR 8.04e- 117 1 PAIA_BACSU PARATHYROID HORMONE PR 8.04e- 117 1 PAIA_BACSU PROTEASE SYNTHASE AND 1.98e- 118 1 PLAK_MOUSE JUNCTION PLAKOGLOBIN ( 3.95e- 118 1 PLAK_MOUSE JUNCTION PLAKOGLOBIN ( 3.95e- 118 1 PLAK_HUMAN JUNCTION PLAKOGLOBIN ( 3.95e- 118 1 PHAP_PHYPO SPHERULIN 1A PRECURSOR 6.98e- 118 1 PHAP_MOUSE PATRADIOL 17 BETA-DEHY 6.98e- 118 1 PHAP_SCOLI PROTEIN ( 1.22e- 118 1 PSTA-ECOLI PROTEIN CHAPT SHOCK PROTE 1.22e- 118 1 HS47_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PROTE 1.22e- 118 1 CBP2_HUMAN ( 47 KD HEAT SHOCK PRO	40	40	41	41	41	41	41	41	41	41	42	42	43	43	43	43	44	48	53	53	53	53	53	Score	
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PTHY_BOVIN PARATHYROID HORMONE PR 8.04e- PTHY_CANFA PARATHYROID HORMONE PR 8.04e- PTHY_PIG PARATHYROID HORMONE PR 8.04e- PTHY_HUMAN PARATHYROID HORMONE PR 8.04e- PAIA_BACSU PROTEASE SYNTHASE AND 1.98e- PLAK_MOUSE JUNCTION PLAKOGLOBIN (3.95e- PLAK_MOUSE JUNCTION PLAKOGLOBIN (3.95e- PLAK_MOUSE JUNCTION PLAKOGLOBIN (3.95e- PLAK_HUMAN JUNCTION PLAKOGLOBIN (3.95e- PAIA_PHYPO SPHERULIN 1A PRECURSOR 6.98e- SRIA_PHYPO SPHERULIN 1A PRECURSOR 6.98e- PHIA_ECOLI PYRUVATE FORMATE-LYASE 1.22e- PFILA_ECOLI PYRUVATE FORMATE-TYASE 1.22e- HS47_KART 47 KD HEAT SHOCK PROTE 1.22e- HS47_HUMAN 47 KD HEAT SHOCK PROTE 1.22e- HS47_HUMAN 47 KD HEAT SHOCK PROTE 1.22e- CBP2_HUMAN COLLAGEN-BINDING PROTE 1.22e- CPT1_MOUSE WITOCHONDRIAL CARNITIN 2.11e- VPR_HYINS VPR PROTEIN (R ORF PRO 2.11e-	96	40	418	417	417	417	405	386	245	105	381	246	1021	743	738	621	585	171	115	115	115	115	115	Length	
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	VPR PROTEIN (R ORF PRO	MITOCHONDRIAL CARNITIN		HEAT SHOCK	HEAT SHOCK	HEAT SHOCK	HEAT SHOCK	PROTEIN C17/B23.			17	1A	111.7				HYPOTHETICAL ABC TRANS		HORMONE	HORMONE	O	HORMONE	HORMONE	Description	
				1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01		1.22e+01											.04e-	.04e-			

45	44	43	42	41	40	39	38	37	36	3 5	34	<b>ω</b>	32	31	30	29	28	27	26	25	24
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FA5_HUMAN	GP21_RAT	LMA3_HUMAN	YSPL_CAEEL	DISA_TRIGA	CCA_HAEIN	AROB_BACSU	RCEM_ERYSP	YG29_YEAST	Y07H_MYCTU	VIF_HV2D1	YOHD_ECOLI	YE11_HAEIN	Y315_METJA	RRPL_RDV	CPT1_RAT	YQZ2_CAEEL	Y187_MYCPN	Y240_MYCGE	Y240_MYCPN	PCXA_ACICA	Y088_METJA
COAGULATION FACTOR V P	INTEGRAL MEMBRANE GLYC	LAMININ ALPHA-3 CHAIN	HYPOTHETICAL 91.0 KD P	PUTATIVE VENOM METALLO	TRNA NUCLEOTIDYLTRANSF	3-DEHYDROQUINATE SYNTH	REACTION CENTER PROTEI	HYPOTHETICAL 34.0 KD P	HYPOTHETICAL TRANSCRIP	VIRION INFECTIVITY FAC	HYPOTHETICAL 21.4 KD P	HYPOTHETICAL PROTEIN H	HYPOTHETICAL PROTEIN M	RNA-DIRECTED RNA POLYM	MITOCHONDRIAL CARNITIN		HYPOTHETICAL ABC TRANS	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	PROTOCATECHUATE 3,4-DI	HYPOTHETICAL PROTEIN M
3.60e+01	3.60e+01		3.60e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01										

2 2	R	P. S	R R	RX ?	0 X	P.	R≱ :	RA S	장	RN	RL :	R S	V F	7 Z	RL	RA	РX	ŖΡ	R	진 3	R 7	2 7	RN	RL	RA	RΑ	RX	RP :	2 6	36	8 6	8 g	DE	Dī	ij,	3 ?	3 8	RESULT
MEDLINE; 71063634.	OF 32-115		AURHACH G D. DOTTS T TR :		ğ			HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,		[5]		F. KISSIL M.S.	MEDITUE: 84.362.8:::	SECTION PROM N A	. CELL. ENDOCRINOL. 28:	ER C.A., GORDON D.F.,	83105964.	UENCE			F KEMPER B	ABRITANCE EXCENT.A.		PROC. NATE. ACAD. SCI. U.S.A. 76:4981-4985(1979).	J.T. JR., RICH A.;	_		SEQUENCE FROM N.A.	[1] ביייייייייייייייייייייייייייייייייייי	EUKARXOTA; METAZOA) CHOKDATA; VEKTEBKATA; TETKAPODA; MAMMALIA; EUHHEBETA, ABHITODACHVIA	(BOVENE).	TATIONS (BOWTNE)	HORMONE PR	(REL. 35, LAST ANNOTATIO		(RET. 01	PTHY_BOVIN STANDARD; PRT; LL5 AA.	1

BREWER H.B. JR., RONAN R.; PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).

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, PTHY_CANFA STANDARD;
2 P52212;
3 P52212;
T 01-0CT-1996 (REL. 34, CREATED)
JT 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                Query Match
Best Local S
Matches
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RA POTTS J.T. JR., TRECEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., DEBTOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

RA DEBTOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

RA DEBTOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

RAC DETTOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

RAC DETTOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

RAC PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

CC C. T. FUNCTION FUTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN CC.

BONE AND PREVENTING THEIR RENAL EXCRETION.

CC C. DONE AND PREVENTING THE SALTS IN C. DONE OF COLUMN THE SALTS IN C. DONE OF C. DONE O
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Best Local Similarity 100.0%;
Matches 7; Conservative
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PROPEP
CHAIN
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-PARATHYROID;
MEDLINE; 95389696;
MEDLINE; 95389696;
ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
DEWILLE J.W., CAPEN C.C.;
GENE 160:241-243(1995).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL; 015662; G558916; ---
PROSITE; PS00335; PARATHYROID; 1.
HORMONE; SIGNAL.
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HORMONE: SIGNAL.
SIGNAL 1
PROPEP 26
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CONFLICT
SEQUENCE
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANIS FAMILIARIS (DOG).
EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; CARNIVORA.
                                      40 HNLGKHL 46
                                                                                                     Local Similarity
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115 AA;
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llarity 100.0%;
Conservative
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32
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31
115 PARATHYROID HORMONE.
106 V -> G (IN REF. 4).
AA; 12980 MW; 673EA5F2 CRC32;
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31
B
115
P
12957 MW;
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BY SIMILARITY.
PARATHYROID HORMONE.
W; 16ED0EBC CRC32;
                                                                          Score 53; DB 1; L
Pred. No. 8.04e-03;
0; Mismatches 0
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Pred. No. 8.04e-03;
0; Mismatches 0; Indels
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Search completed: Thu Jul 30 10:30:06 1998 Job time : 5 secs.

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Title:
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                                                                                                                                                                                                                       protein - protein database search, using Smith-Waterman algorithm
>US-08-817-547A-15
(1-7) from US08817547A.pep
53
1 HNLGKHL 7
                                                                                                                                               Thu Jul 30 10:30:24 1998; MasPar time 3.61 Seconds 81.661 Million cell updates/sec
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Tabular output not generated.

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Database: Post-processing: Minimum Match 0% Listing first 45 summaries

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 20.260; Variance 20.374; scale 0.994

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

19 40 75	17 41 77				42		42	42	42	8 43 81		6 43 81	5 43 81	4 43 81	3 44 83	2 48 90	1 53 100	No. Score Match	æ
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CARNITHINE PALMITOYLIR	HYPOTHETICAL 62.3 KD P	SHOCK	31.3 K	HYPOTHETICAL 110.0 KD	CHROMOSOME XV READING	THYMIDYLATE SYNTHASE,	17-BETA HYDROXYSTEROID	WNT-LIKE PROTEIN WNT14	VPR PROTEIN.	KIAA0302 (FRAGMENT).	PLAKOGLOBIN.	PLAKOGLOBIN.	COSMID T07E3.	PLAKOGLOBIN (FRAGMENT)	VPR PROTEIN.	TRANSCRIPTIONAL REGULA	PARATHYROID HORMONE (F	Description	
3.12e+01	1.82e+01	1.82e+01	1.82e+01	1.05e+01	1.05e+01	1.05e+01	1.05e+01	1.05e+01	1.05e+01	5.98e+00	5.98e+00	5.98e+00	5.98e+00	5.98e+00	3.38e+00	3.17e-01	1.38e-02	Pred. No.	

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[1] SEQUENCE FROM N.A. STRAIN-168; KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G., AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,	PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.	(TREMBLREL: 05, (TREMBLREL: 05, ONAL REGULATOR.	32112; 32112;	30 HNLGKHL 36         1 HNLGKHL 7	Query Match 100.0%; Score 53; DB 10; Length 105; Best Local Similarity 100.0%; Pred. No. 1.38e-02; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE-THYROID, AND PARATHYROID;  TISSUE-THYROID, AND PARATHYROID;  TISSUE-THYROID, AND PARATHYROID;  TISSUE-THYROID, AND PARATHYROID;  APPLIA GRIEF TECHNOL. 21:228-229(1984).  EMBL; M54875; G601933;  NON_TER 1 1 1  NON_TER 1 1 1  SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;	PIA. RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. [1]	LT 1 Q63473 PRELIMINARY; PRT; 105 AA. Q63473; Q1-NOV-1996 (TREMBLREL. 01, CREATED) Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) PARATHYROID HORMONE (FRAGMENT).

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RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
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RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C.,
RA GLASER P., GOFFERN A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G., GUY B.J.,
RA HAGA K., HAIECH J., HARWOOD C.R., HENAUT A., HILBERT H., HOLSAPPEL S.,
RA KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYLSHI Y., KOETTER P.,
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RA MOESTL D., NARAI S., NOBACK M., NOONE D., O'REILLY M., OGAWA K.,
RA PORWOLLIK S., PRESCOTT A.M., PRESECAN E., PUJIC P., PURNELLE D.,
RA ROCHE B., ROSE M., SADAIE Y., SATO T., SCANLAN E., SCHLEEICH S.,
RA SCHROETER R., SCOFFONE F., SERIGUCHI J., SEKOWSKA A., SEROR S.J.,
SERROR P., SHIN B.S., SOLDO B., SOROKIN A., TAKEUCHI M., TAMAKOSHI A., TANAKA T.,
VANUERES P., VASSAROTTI A., VIARI A., WEDLER E., WEDLER H.,
RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMJEENDL M.,
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Matches 6; Conservation
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SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z99120; E1184294; -.
SEQUENCE 172 AA; 20015 MW; 2AA7F8CE CRC32;
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Psrch_pp 85 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:33:38 1998;

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Title:

Sequence: Perfect Score: Description: >US-08-817-547A-16 (1-6) from US08817547A.pep 45 1 HNLGKH 6

Scoring table:

Searched: PAM 150 Gap 15 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
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Statistics: Mean 13.446; Variance 33.754; scale 0.398

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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04-APR-1996.
28-SEP-1994; 434551.
28-SEP-1994; DE-434551.
R88840;
07-OCT-1996 (first entry)
07-OCT-1996 (first entry)
Human parathyroid hormone analogue, [Leu27]-hPTH(1-32)-NH2.
Parathyroid hormone; PTH; analogue; osteoporosis; bone cell
Parathyroid regulation; reduced PKC activity; protein kinase C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 96-180391/19.

New antigenic peptide(s) from human parathyroid hormone - and antibodies generated using them, able to distinguish between active and inactive forms of the hormone

Claim 2; Page 5; 5pp; German.

The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- occ-terminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting an animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37).

Sequence 9 AA;
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06 NOV-1996 (first entry)
Human parathyroid hormone antigenic peptide hPTH 9-17.
Human parathyroid hormone; hPTH; antigen; alpha-helix;
diagnosis; active hPTH 1-37.
                                                                                                                                                                                                               R88840 standard; peptide;
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PD 21-DEC-1995.

PP 20-JUN-1994; 126299.

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PR 20-JUN-1994; CA-126299.

PR 20-JUN-1994; CA-126299.

PR (WILL/) WILLICK G E.

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

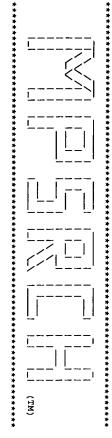
PI Willick GE;

PR WPI; 96-151754/16.

PT New human parathyroid hormone analogues - which have increased adenylyl cyclase activating activity, used for treating osteoporosis Claim 2; Page -; 21pp; English.

CR 88829-R88841 are human parathyroid hormone (hPTH) analogues. The Standogues increase G-protein coupled adenylyl cyclase (cAMPase) canalogues increase G-protein kinase C (PKC) activity. The analogues without undesirable effects. They are useful for the treatment of involving bone cell calcium regulation.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      increased adenylyl cyclase activity; cAMPase; bone loss.
Synthetic.
Key
Location/Qualifiers
                                                                  9 hnlgkh 14
||||||
1 HNLGKH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 32 /note= "amidated"
                                                                                                                             Score 45; DB 18; Length 32;
Pred. No. 1.82e+01;
0; Mismatches 0; Indels
                                                                                                                               0;
                                                                                                                             Gaps
                                                                                                                             0;
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Apsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:33:02 1998; MasPar time 3.01 Seconds 72.782 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-16 (1-6) from US08817547A.pep 45 1 HNLGKH 6

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 18.479; Variance 19.656; scale 0.940

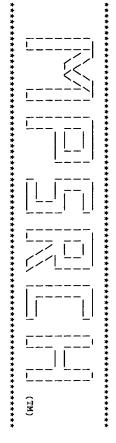
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

NO.	Score	Query Match	Length	BB	ij	Description	Pred. No
<b>–</b>	45	100.0	34	5	1ZWG	parathyroid hormone 4	5.80e-01
N	45	100.0	34	σ	12WF	_	5.80e-01
ω	45	100.0	34	u	1ZWE	parathyroid hormone (	
4	45		34	տ	1ZWA	_	5.80e-01
σ	45	100.0	35	σ	12WD	_	5.80e
σ	45	100.0	36	σ	1ZWB	parathyroid hormone (	5.80e
7	45	100.0	37	υı	1HPH	parathyroid hormone f	5.80e-01
8	45	100.0	37	G	1ZWC	parathyroid hormone (	5.80e-01
ø	45	100.0	105	N	151851	parathyroid hormone -	5.80e-01
10	45	100.0	115	N	JC4202	_	5.80e-01
11	45	100.0	115	N	A05091	parathyroid hormone p	5.80e-01
12	45	100.0	115	1	PTHU	parathyroid hormone p	5.80e-01
13	45	100.0	115	_	PTBO	parathyroid hormone p	5.80e-01
14	45		115	H	PTPG	parathyroid hormone p	5.80e-01
15	43	95.6	1021	N	S44644	F37A4.7 protein - Cae	1.85e+00
16	42	93.3	34	u	1HTH	010	3.28e+00
17	41	91.1	246	N	S01789	pyruvate formate-lyas	5.74e+00
18	40		172	N	A35145	transcriptional regul	9.97e+00
19	40	-	172	N	E69671	transcriptional repre	9.97e+00
20	39		264	N	A64637	hypothetical protein	1.72e+01
21	39		386	N	D42528	B23R protein - vaccin	1.72e+01
22	39		480	۳	A30065	trigramin precursor -	1.72e+01
23	37	ာ ၁	2				

36	36	36	36	36	36	36	36	36	37	35 37	37	37	37	37	37	37	37	37	37	37	37
•	•	•	•	•	•	•	٠	•	•	82.2	•	•	٠	٠	•	•	•	٠	•	•	•
1209	933	700	586	540	403	390	123	60	1969	1966	1947	1938	1097	633	534	330	232	119	116	116	116
2	N	N	2	۳	N	N	N	N	۳	۳	۲	۳	N	N	N	ب	N	Ν	N	μ	N
A49440	S53523	JH0162	S73346	OYHUCR	в69196	в37059	S75382	E69209	S02771	MWKW	S05697	MWKW1	A29943	JQ1242	S61228	WNBCM	146679	A34937	S13965	NGNJXI	A58566
chromosome disjunctio	methylenetetrahydrofo	No-on-transient A pro	sn-glycerol-3-phospha	natriuretic peptide r	conserved hypothetica		hypothetical protein	conserved hypothetica		heavy chain			Toll protein precurso	Viral replicase 2 - b	DNA (cytosine-5-)-met	photosynthetic reacti	h muscle	5	nerve growth factor -		nerve growth factor -
		٠	8.24e+01	8.24e+01	8.24e+01		8.24e+01	8.24e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01

#book	REFERENCE	#submission submitted to #cross-references PDB:12WF	#authors	ORGANISM	ALTERNATE_NAMES PDB_TITLE	TITLE	RESULT 2	Qy 1 HNLGKH	Db 6 HNLGKH	Query Match Best Local Sim Matches 6;	SUMMARY	15-25	FEATURE	<b>U</b> 2	COMMENT Resol	#000K	#authors	REFERENCE TNO	#submission	#authors	REFERENCE	G (	ATTERNATE NAMES	TITLE	RESULT 1
in Strukturen Verschiedener Parathormonfragmente in Loesung,	TN003318	submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:12WF	Marx, U.C.	10 structures 1_name synthetic	<pre>synthetic n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone,</pre>	parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -		a	11	Query Match 100.0%; Score 45; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 5.80e-01; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#length 34 #molecular-weight 4128 #checksum 5508	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha)\</pre>		disease mutation: hormone: signal		nn.O. Bavrenth : University of Bavrenth /Thesis). 1996	-	INO03319	nitte	Roesch, P.; Marx, U.C.	#IDIMAI_name Synthetic A67743	succinyl human parathyroid hormone 4-37, NMR, 10 structures		12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:31:49 1998; MasPar time 2.04 Seconds 73.883 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-16 (1-6) from US08817547A.pep 45 1 HNLGKH 6

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 19.288; Variance 15.923; scale 1.211

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 5 5 5 6 6 6 6 7 7 6 6 1 1 1 1 1 1 1 1 1 1 1 1	gult No:
37 37 37 37 37 37 37 37 37 37 37	Score
100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00	Query Match
115 115 115 115 115 115 1021 1021 1021 1	Length
	B
PTHY_BOVIN PTHY_CANFA PTHY_RIG PTHY_RIG PTHY_HUMAN YPT7_CAEELL PFLA_ECOLI YBXF_STAAU VC17_VACCC DISA_TRIGA YPR_HV1N5 YPR_CAEELL NGE_NAJAT NGF_NAJNA PTHY_CHICK PADI_SCHPO RCEM_ERYSP MYSA_CAEELL MYSC_CAEELL MYSA_CAEELL MYSA_CAEELL MYSA_CAEELL MYSA_CAEELL	ID
PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PYRUVATE FORMATE-LYASE PROBABLE RIBOSOMAL PRO PROTEASE SYNTHASE AND PROTEIN C17/B23. PUTATIVE VENOM METALLO VPR PROTEIN (R ORF PRO VPR PROTEIN (R ORF PRO VPR PROTEIN (R ORF PRO VPR PROTEIN HORMONE PR NERVE GROWTH FACTOR (N NERVE	Description
4.76e-02 4.76e-02 4.76e-02 4.76e-02 4.76e-02 4.76e-02 2.00e-01 8.04e-00 1.58e+00 3.08e+00 3.08e+00 3.08e+00 3.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01	Pred. No.

4.4 5	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
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	77.8			77.8	77.8	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	•	•	80.0	•	•	80.0	80.0
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PUR2_CHITE	GUTR_BACSU	PLAK MOUSE	ZN12_MICSA	COND_NEUCR	RL1_THETH	YJ03_YEAST	THR_DROME	SRE1_HUMAN	DPOM_CLAPU	KDPD_ECOLI	NONA_DROME	RIP_HUMAN	Y719_METJA	Y187_MYCPN	Y187_MYCGE	ANPC_HUMAN	KCRB_CHICK	KCRB_HUMAN	NEF_SIVAG	Y4KH_RHISN
PHOSPHORIBOSYLAMINEG :	Ö.	TION PLAKOGLOBIN (	ZINC FINGER PROTEIN ZF :	CONIDIATION-SPECIFIC P :	50S RIBOSOMAL PROTEIN :	HYPOTHETICAL 154.9 KD	THREE ROWS PROTEIN.	STEROL REGULATORY ELEM :	PROBABLE DNA POLYMERAS :	SENSOR PROTEIN KDPD (E :	NO-ON-TRANSIENT A PROT :	SERINE/THREONINE PROTE :	HYPOTHETICAL ABC TRANS :	HYPOTHETICAL ABC TRANS :	HYPOTHETICAL ABC TRANS :	ATRIAL NATRIURETIC PEP :	CREATINE KINASE, B CHA :	CREATINE KINASE, B CHA :	NEGATIVE FACTOR (F-PRO :	HYPOTHETICAL 14.1 KD P :
3.82e+01 3.82e+01			3.82e+01	3.82e+01	3.82e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01

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RESULT ID PT AC PE DT 01 DT 01 DT 01 DT 01 DT 02 DT 02 DT 02 DT 03 DT 03 DT 04 DT 05 DT 05
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                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
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A DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
L. PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
C. -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL; VO0106; 685; -.
DR EMBL; J00024; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18250; ALT_INIT.
BEBL; J00024; E18250; ALT_INIT.
DR EMBL; K01938; G163645; -.
DR EMBL; K01938; G163645; -.
DR EMBL; K01938; G163645; -.
DR EMBL; NOTSAL DREG
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-PARATHYROID;
MEDLINE: 95369696.
ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
DEWILLE J.W., CAPEN C.C.;
GENE 160:241-243(1995).
-!- FUNCTION: PTH ELEVATIES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
EMBL; U15662; G558916; -.
PROSITE: PS00335; PARATHYROID; 1.
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                           HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANIS FAMILIARIS (DOG).
EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CARNIYORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTHY_CANFA STANDARD; PRT; 115 AA. P52212; 01-0CT-1996 (REL. 34, CREATED) 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HORMONE; SIGNAL.

SIGNAL 1 25

PROPEP 26 31

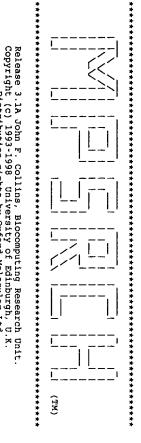
CHAIN 32 115

CONFLICT 106 106

V -> G (IN REF. 4).

SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;
                           40 HNLGKH 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A01534; PTBO.
PIR; A24949; A2494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BREWER H.B. JR., RONAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
1 HNLGKH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 HNLGKH 45
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26
32
115 AA;
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                                                                                                                                                                                              25 B
31 B
115 P
; 12957 MW;
                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
W; 16ED0EBC CRC32;
                                                                                 Score 45; DB 1; Length 115;
Pred. No. 4.76e-02;
0; Mismatches 0; Indels
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Pred. No. 4.76e-02;
0; Mismatches 0; Indels
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Search completed: Thu Jul 30 10:31:56 1998 Job time: 7 secs.



MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:32:12 1998; MasPar time 3.65 Seconds 69.257 Million cell updates/sec

Title: Tabular output not generated. >US-08-817-547A-16 (1-6) from US08817547A.pep 45

Description: Perfect Score: Sequence: 1 HNLGKH 6

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb15

1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

Statistics: Mean 18.554; Variance 16.504; scale 1.124

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

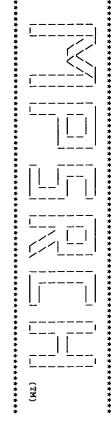
Result No.	Score 45	Query Match 100.0 93.3	Length 105 96	110	ID Q63473 Q72500	Description PARATHYROID HORMONE (F
<b>ω</b> 4	4 4	88.9 .9	96 172	11	P88152	VPR PROTEIN.
<b>σ</b> ,	39	86.7		9	025591	•
თ	39	86.7	453	1	Q83077	IN.
7	39	86.7	480	12	Q90220	PREPRO-HALYSTATIN PREC
œ	38	84.4	96	11	Q79793	ISOLATE NY5, COMPLETE
9	38	84.4	96	11	Q79249	VPR PROTEIN.
10	38	84.4	96	H	Q79233	VPR PROTEIN.
11	38	84.4	348	œ	Q42966	NITRILASE (EC 3.5.5.1)
12	37	82.2		9	Q54077	I GI:
13	37	82.2	95	11	074777	ISOLATE 891-1, VPR.
14	37	82.2	107	4	018840	GAMMA ACTIN.
15	37	82.2	184	9	030668	ACID SHOCK PROTEIN.
16	37	82.2	232	4	Q95210	ALPHA-SMOOTH MUSCLE AC
17	37	82.2	308	ᆫ	010278	K-252A-RESISTANCE PROT
18	37	82.2	534	9	Q60171	MODIFICATION METHYLASE
19	37	82.2	591	ω	022545	T18D3.4 (FRAGMENT).
20	37	82.2	633	•	00000	

ROWS PROTEIN.	THREE	Q94525	ω	1209	80.0	36	45
HYPOTHETICAL PROTEIN.	HYPOTH	022864	œ	947	•	36	44
<b>METHYLENETETRAHYDROFOL</b>	METHYLI	Q27772	w	933	•	36	43
OTEIN.	BJ6 PROTEIN.	Q24261	ω	700	80.0	36	42
-ALPHA-GLUCANOTRANSFE	4-ALPH	032462	9	659	•	36	41
GENASE (FRAGMENT	LIPOXYGENASE	Q41520	œ	517		36	40
COSMID F59E12.	COSMID	001906	ω	414	•	36	39
55151	FROM BASES	P77444	ဖ	406		36	38
TINE KINASE (EC	B-CREATINE	Q92061	12	376	•	36	37
PROTEIN.		P90269	11	210	•	36	36
(NEF).	NEF (NI	Q75738	11	206	•	36	35
(NEF).	NEF (NI	Q75728	11	206	•	36	34
EF).	NEF (NEF	Q75746	11		•	36	ω ω
NEF).	NEF (NI	Q75732	11		•	36	32
	NEF.	Q74919	11		•	36	31
	NET.	Q74920	11			36	30
C04015.	ORF CO	P95954	9	123	•	36	29
PROTEIN.	A670R I	041152	11		•	36	28
1.	K12F2.1.	021440	ω		•	37	27
SIMILARITY TO C. ELEGA	SIMILA	021000	ω		•	37	26
4 (FRAGMENT).	T18D3.4	Q20439	ω		•	37	25
ROTEIN.	TOLL PROTEIN	Q24622	ω		•	37	24
3 (FRAGMENT).	F11C3.	002244	w		•	37	23
<pre>10 (FRAGMENT).</pre>	R06C7.	Q19674	ω	892	82.2	37	22
	ORF3.	Q65875	1		•	37	21

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IRESULT
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AC Q7
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Matches
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Q72500
Q72500;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1996
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -
NON_TER 1
                                         HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
LENTIVIRINAE.
                                                                                     VPR PROTEIN.
MEDLINE; 96036482
            STRAIN-NL4-
                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                      PARATHYROID
                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; RODENTIA.
                                                                                                                                                                                                                             y Match 100.0%;
Local Similarity 100.0%;
hes 6; Conservative
                                                                                                                                                                                               30 HNLGKH 35
                                                                                                                                                                                    1 HNLGKH 6
                                                                                                                                                                                                                                                                        105 AA; 11746 MW;
                                                                                             (TREMBLREL. 01, 05 (TREMBLREL. 01, 05)
                                                                                                                                                                                                                                                                                                                                                                                                               (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                      HORMONE (FRAGMENT).
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                        Score 45; DB 10;
Pred. No. 1.06e-01;
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                        6AC3163E CRC32;
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                                                                                                                                          96
                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                  Length 105;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                              0
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                              0;
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RA SALMINEN M.O., KOCH C., SANDERS-BUELL E., EHRENBERG P.K.,
RA MICHAEL N.L., CARR J.K., BURKE D.S., MCCUTCHAN F.E.;
RI VIROLOGY 213:80-86(1995).
RP SEQUENCE FROM N.A.
RC STRAIN-NAL4-3;
RX MEDLINE; 86281827.
RA ADACHI A., GENDELMAN H.E., KOENIG S., FOLKS T., WILLEY R.,
RA ADACHI A., GENDELMAN H.E., KOENIG S., FOLKS T., WILLEY R.,
RA ADACHI A., GENDELMAN H.E., KOENIG S., FOLKS T., WILLEY R.,
RL J. VIROL. 59:284-291(1986).
RL J. VIROL. 59:284-291(1986).
FT COMPLICT 44
RABSON A., MARTIN M.A.;
FT COMPLICT 44
REMBL; U26942; G902802; -.
FT COMPLICT 44
SO SEQUENCE 96 AA; 11391 MW, 035C4D75 CRC32;
Ouery Match
Best Local Similarity 83.3%; Pred. No. 8.18e-01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGRH 45
1 HNLGRH 45
1 HNLGRH 6
Search completed: Thu Jul 30 10:32:45 1998
Job time: 33 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:36:04 1998; MasPar time 2.57 Seconds 29.790 Million cell upda cell updates/sec

Tabular output not generated

Description: Perfect Score: Title: (1-5) from US08817547A.pep 36 1 HNLGK 5 >US-08-817-547A-17

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match Listing first 0% 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.815; Variance 28.014; scale 0.457

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

114321110 114321110 1143211110	Result
๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛ ๑๑๑๑๑๑๑๑๑๑๑๑๑๑๑๑๑๑๑๑	Score
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111222 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	80
R52139 R58189 R41568 R41568 R58187 R34455 R34457 W17953 W17953 W17957 R74490 R74489 R74489 R74489 R58055 R58066 R58166 R58166 R58166 R58166 R58166 R58166	ij
Accelerator peptide b [F23,H25,H26,L27,I28, [Lys15,16 H1s27]hpTH [Phe23,H1s25,H1s26,Le Bovine parathyroid hor Human parathyroid hornone p Parathyroid hornone p Parathyroid hornone p [L8,A16,Q18,A19,R22]-[L6,Q18]-hpTH(1-36)-NH [Pr33]-hpTH(1-36)-NH [Pr33]-hpTH(1-38)-OH [I1e33]-hpTH(1-38)-OH [I1e15]-hpTH(1-38)-OH [I1e15]-hpTH(1-38)-OH [I1e15]-hpTH(1-38)-OH [A1a19]-hpTH(1-38)-OH [A1a19]-hpTH(1-38)	Description
1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02	Pred. No.

36 100.0 38 9 R58124 [Val14]-hPTH(1-38)-OH 36 100.0 38 9 R58108 [Arg14]-hPTH(1-38)-OH 36 100.0 38 9 R58078 [Arg14]-hPTH(1-38)-OH 36 100.0 38 9 R58078 [Gly33]-hPTH(1-38)-OH 36 100.0 38 9 R58078 [Gly33]-hPTH(1-38)-OH 36 100.0 84 4 R23430 Porcine parathyroid hor 36 100.0 84 4 R23433 Bovine parathyroid hor 36 100.0 84 4 R23422 Porcine parathyroid hor 36 100.0 84 4 R23423 Porcine parathyroid hor 36 100.0 84 4 R234313 Porcine parathyroid hor 36 100.0 84 4 R23432 Porcine parathyroid hor 36 100.0 84 5 R29562 Oxidation resistant [ R2346] Stability enhanced hu 36 100.0 84 4 R23347 Bovine parathyroid hor 36 100.0 84 4 R23349 Bovine parathyroid hor 36 100.0 84 4 R23349 Bovine parathyroid hor 36 100.0 84 4 R23281 Bovine parathyroid hor 36 100.0 84 4 R23485 Porcine parathyroid hor 36 100.0 84 4 R23487 Porcine parathyroid hor 36 100.0 84 4 R23477 Porcine parathyroid hor 36 100.0 84 4 R23475 Porcine parathyroid hor 36 100.0 84 4 R23477 Porcine parathyroid hor 36 100.0 84 4 R23475 Porcine parathyroid hor 36 100.0 84 4 R23475 Porcine parathyroid hor 36 100.0 84 4 R23495 Porcine parathyroid hor 36 100.0	45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
00.0 38 9 R58124 [Lys1y]-nPTH(1-38)- 00.0 38 9 R58105 [Arg14]-hPTH(1-38)- 00.0 38 9 R58108 [Arg14]-hPTH(1-38)- 00.0 38 9 R58078 [Leu33]-hPTH(1-38)- 00.0 38 9 R58078 [Gly33]-hPTH(1-38)- 00.0 44 26 P30015 Human parathyroid h 00.0 84 4 R23439 Porcine parathyroid 00.0 84 4 R23363 Bovine parathyroid 00.0 84 4 R23363 Porcine parathyroid 00.0 84 8 R42069 Stability-enhanced 00.0 84 8 R42069 Stability-enhanced 00.0 84 8 R42069 Stability-enhanced 00.0 84 8 R33429 Porcine parathyroid 00.0 84 8 R3343 Bovine parathyroid 00.0 84 4 R23349 Bovine parathyroid 00.0 84 4 R23349 Bovine parathyroid 00.0 84 4 R23385 Porcine parathyroid 00.0 84 4 R23385 Porcine parathyroid 00.0 84 4 R23385 Porcine parathyroid 00.0 84 4 R23361 Bovine parathyroid 00.0 84 4 R23361 Human parathyroid 00.0 84 4 R23163 Human parathyroid h 00.0 84 4 R23477 Porcine parathyroid 00.0 84 4 R23475 Porcine parathyroid 00.0 84 4 R23405 Porcine parathyroid	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	ω 6	36	36	36
8 9 RS8124 [Lys1y]-nPTH(1-38)- 8 9 RS8108 [Arg14]-hPTH(1-38)- 8 9 RS8108 [Arg14]-hPTH(1-38)- 8 9 RS8077 [Leu33]-hPTH(1-38)- 8 9 RS8077 [Leu33]-hPTH(1-38)- 8 9 RS8077 [Cly33]-hPTH(1-38)- 4 26 P30015 Human parathyroid h 4 27 WZ5687 Human parathyroid h 4 R23433 Bovine parathyroid 4 R23433 Bovine parathyroid 4 R23463 Forcine parathyroid 4 R23469 Stability-enhanced 5 R29562 Oxidation resistant 6 R2069 Stability-enhanced 7 R29561 Oxidation resistant 8 R2067 Bovine parathyroid 9 R23349 Porcine parathyroid 9 R23349 Porcine parathyroid 1 R23347 Bovine parathyroid 1 R23477 Bovine parathyroid 1 R23477 Porcine parathyroid 1 R23477 Porcine parathyroid 1 R23477 Porcine parathyroid 1 R23477 Porcine parathyroid 1 R23476 Porcine parathyroid 1 R23477 Porcine parathyroid 2 R23477 Porcine parathyroid	8	8	8	8	8	8	80.	8	8	8	8	8	8	8	8	80.	8	8	8	8	8	80.	80.	80.	8	00.
9 K58124 [Lys1y-nPH(1-38) 9 K58106 [Arg14]-hPH(1-38) 9 K58077 [Leu33]-hPH(1-38) 9 K58078 [Gly3]-hPH(1-38) 9 K58078 [Gly3]-hPH(1-38) 7 W25687 Human parathyroid h 7 W25687 Human parathyroid h 7 K23430 Porcine parathyroid 4 K23431 Porcine parathyroid 4 K23432 Porcine parathyroid 5 K23413 Porcine parathyroid 6 K42069 Stability-enhanced 6 K29561 Oxidation resistant 6 K29561 Oxidation resistant 7 K29561 Porcine parathyroid 8 K23349 Porcine parathyroid 8 K23349 Porcine parathyroid 8 K23349 Porcine parathyroid 8 K23274 Bovine parathyroid 8 K23485 Porcine parathyroid 8 K23485 Porcine parathyroid 8 K234876 Porcine parathyroid 8 K23477 Porcine parathyroid 8 K23477 Porcine parathyroid 8 K23477 Porcine parathyroid 8 K23477 Porcine parathyroid 8 K23405 Porcine parathyroid	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	44	38	3 8	38	38	ğ
81124 [Lysly]-nPH(1-38)- 8108 [Arg14]-hPH(1-38)- 8108 [Arg14]-hPH(1-38)- 8078 [Gly33]-hPH(1-38)- 8076 parathyroid hose parathyroid hos	4	4	4	4	4	4	4	4	4	4	4	4	ъ	G	8	4	4	4	4	27	26	9	9	9	9	v
prin(1-38)- prin(1	329	340	347	347	116	116	326		1.3								342	3	34	568	2001	807	807	810	810	2TR
	parathyroid	parathyroid	ine parathyroid	ine parathyroid	parathyroid ho	parathyroid ho	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	resistant	resistant	enhanced	ine parathyroid	parathyroid	parathyroid	parathyros	parathyroid	parathyroid	)3]-hPTH(1-38)-	)3]-hPTH(1-38)-	4]-hPTH(1-38)-	4]-hPTH(1-38)-	319]-NFTH(1-38)-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 3; 7pp; Japanese.

The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic amino acids. The accelerat also comprises cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The accelerator is applied by opening the gingiva, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the epithelium and accelerates fibre adhesion and regenerates cement. Sequence 34 AA;
JT 2
JT 2
Standard; peptide; 34 AA.
R58189;
20-SEP-1994 (first entry)
[F23,H25,H26,L27,I28,A29,E30,I31,T33,A34]-hPTH(1-34)-NH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-FEB-1993; JP-045998.
(SUNZ ) SUNSTAR CHEM IND CO LTD.
WPI; 95-157631/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
periodontal tissue; regeneration; periodontitis; periodontal pocket;
down growth; epithelium; fibre adhesion; cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R62432 standard; peptide;
R62432;
31-JUL-1995 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accelerator for regenerating periodontal tissue - peptide having 3-34 aminoacid residues having conn aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1994.
10-FEB-1993; 045998.
10-FEB-1993; JP-0459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J06234653-A.
                                                                                                                                                                                                                                                                              1 HNLGK 5
                                                                                                                                                                                                                                                                                                                              9 hnlgk 13
                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 26;
Pred. No. 1.04e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ue - comprises connected basic
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Search completed: Thu Jul 30 10:36:20 1998 Job time : 16 secs.
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PD 02-FEB-1994

PF 12-UUL-1993; 014384.

PR 15-UUL-1992; GB-015009

PR 23-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026861.

PR 23-DEC-1992; GB-026865.

PR 23-DEC-1992; GB-026865.

PR 23-DEC-1992; GB-026861.

PR 23-DEC-1992; GB-026861.

PR 23-DEC-1992; GB-026861.

PR 23-DEC-1992; GB-026861.

PR 23-DEC-1992; GB-026863.

R-2-DEC-1992; GB-026863.

R-2-DEC-1922; GB-026863.

R-2-DEC-1922; GB-026863.

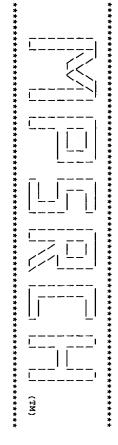
R-2-DEC-1922; GB-026863.

R-2-DEC-1922; GB-026863.

R-2-DEC-1922; GB-026863.

R-2-DEC-1922; GB-02686
                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HNLGK 5
                                                                                                                                                                           9 hnlgk 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; Synthetic.

Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                 Score 36; DB 9; Length 34;
Pred. No. 1.04e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                 0;
                                                                                                                                                                        Gaps
                                                                                                                                                                     0,
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MPsrch_pp 9 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:35:29 1998; MasPar time 2.99 Seconds 61.109 Million cell updates/sec

Sabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-17 (1-5) from US08817547A.pep 36 1 HNLGK 5

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 17.484; Variance 16.519; scale 1.058

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

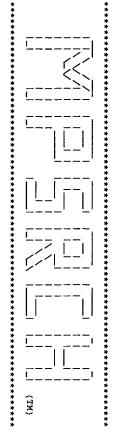
#### SUMMARIES

No.	Score	Query Match	Length I	В	Ħ	Description	Pred. No.
۳	36	100.0	34	5	1ZWG	parathyroid hormone 4	1.89e+01
N	36	100.0	34	u	12WF		1.89e+01
ω	36	100.0	34	u	12WE	parathyroid hormone (	
4	36	100.0	34	u	1ZWA	parathyroid hormone (	1.89e+01
υ	36	100.0	35	Ģ	1ZWD	parathyroid hormone (	1.89e+01
σ	36	100.0	36	u	1ZWB	parathyroid hormone (	1.89e+01
7	36	100.0	37	S	1HPH	parathyroid hormone f	1.89e+01
8	36	100.0	37	u	12WC	<pre>parathyroid hormone (</pre>	1.89e+01
ø	36	100.0	105	N	I51851	parathyroid hormone -	1.89e+01
10	36	100.0	115	1	PTPG	parathyroid hormone p	1.89e+01
11	36	100.0	115	N	JC4202	parathyroid hormone -	1.89e+01
12	36	100.0	115	N	A05091	parathyroid hormone p	1.89e+01
13	36	100.0	115	1	PTBO	parathyroid hormone p	1.89e+01
14	36	100.0	115	_	PTHU	parathyroid hormone p	1.89e+01
15	36	100.0	123	N	S75382	$\mathbf{c}$	1.89e+01
16	36	100.0		N	B42372	regulatory protein Kd	1.89e+01
17	36	100.0		N	JQ0301	hypothetical 127K pro	1.89e+01
18	36	100.0		N	S42622	three rows protein -	1.89e+01
19	36	100.0	1209	N	A49440	chromosome disjunctio	1.89e+01
20	34	94.4	142	N	C70059	വ	6.05e+01
21	34	94.4	146	Н	нвну	ñ	6.05e+01
22	34	94.4	146	Н	HBOZ	hemoglobin beta chain	6.05e+01
23	34	94.4	146	N	JU0163	hemoglobin beta chain	6.05e+01

45	44	43	42	41	40	39	ထ	37	36	<u>3</u> 5	34	33	32	31	30	29	28	27	26	25	24
33	33	33	33	33	33	ω ω	ω w	34	34	34	34	34	34	34	34	34	34	34	34	34	34
91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7		٠.	٠.	94.4	94.4		94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4
578	274	273	273	147	147	146	34	3135	1021	830	759	711	573	573	573	573	416	412	348	314	147
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E69259	I52851	1QRDB	1QRDA	S34719	HBMS	HBOL	1HTH	A48584	S44644	C69011	G69258	E69953	A34173	HHMS60	A32800	HHRT60	В64132	RNECTA	F69831	G69818	S22336
aldehyde ferredoxin o	NAD(P)H dehydrogenase	quinone-reductase (EC	quinone-reductase (EC	beta		hemoglobin beta chain	cyclic parathyroid ho	transmission-blocking	F37A4.7 protein - Cae	conserved hypothetica	_	775		chaperonin groEL prec	roEL	chaperonin groEL prec	tRNA adenylyltransfer	tRNA adenylyltransfer	iron(III) dicitrate-b	CMP-binding factor ho	hemoglobin beta chain
1.06e+02	1.06e+02	1.06e+02	1.06e+02	1.06e+02	1.06e+02	1.06e+02	1.06e+02	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01

ORGANISM REFERENCE #authors #submission #cross-referore REFERENCE #authors #book	RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE	Db 6 HNLGK       Qy 1 HNLGK	Query Match Best Local Sim. Matches 5;	2-9 15-25 SUMMARY	#authors #book  COMMENT Reso: COMMENT Detes KEYWORDS FEATURE	#authors #submission #cross-refere REFERENCE	ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE	RESULT 1 ENTRY TITLE
#formal_name synthetic BRENCE A67742 BRENCE A67742 #authors Roesch, P.; Marx, U.C. #submission submitted to the Brookhaven Protein Data Bank, June 1996 #cross-references PDB:1ZWF #cross-references PDB:1ZWF TN003318 #BERNCE TN003318 #authors Marx, U.C. #book in Strukturen Verschiedener Parathormonfragmente in Loesung,	1ZWF #type complete parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures	10	1 100.0%; Score 36; DB 5; Length 34; Similarity 100.0%; Pred. No. 1.89e+01; 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR disease mutation; hormone; signal	#authors Roesch, P.; Marx, U.C. #submission submitted to the Brookhaven Protein Data Bank, June 1996 #cross-references PDB:1ZWG ERENCE TN003319	n-succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic A67743	1ZWG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -

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COMMENT
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MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:34:11 1998; masPar time 2.00 Seconds 62.590 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-17 (1-5) from US08817547A.pep 36 1 HNLGK 5

Description: Perfect Score: Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 18.208; Variance 13.355; scale 1.363

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU DEFTOS L.J., DAMSON B.F., HOGAN M.L., AIRBACH G.D.;

PROC. NATL. ACAD. SCI. U.S. A. 68:63-67(1971).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE S
BONE AND PREVENTING THEIR RENAL EXCRETION.

R EMBL; V00106; 685; -.

R EMBL; J00024; G163641; -.

R EMBL; J00024; G163643; -.

R EMBL; J00024; G163645; -.

R EMBL; J00024; E18250; ALT_INIT.

R EMBL; J00024; G163647; -.

R EMBL; K01938; G163645; -.

RR EMBL; K01938; G163645; -.
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PROSITE;
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POTTS J.T. JR.;
BIOCHEMISTRY 13:1994-1999(1974).
-!-FUNCTION: PTH ELEVARES CALCIUM LEVEL BY DISSOLVING THE SALTS
BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL; X05722; G1839; -.
PIR; A01535; PTPG.
PIR; B26806; B26806.
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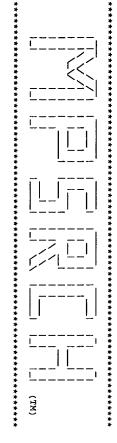
MEDILINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE
BIOCHEMISTRY 14:3631-3635(1975).

[3]
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HORMONE; SIGNAL.
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MEDLINE; 87316938.
SCHMELZER H.-J., GROSS G., WIDERA G., SCHMELZER ACIDS RES. 15:6740-6740(1987).
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SUS SCROFA (PIG).
EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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MEDLINE; 74253317.
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01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
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V: 12980 MW;
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. on: Thu Jul 30 10:34:37 1998; MasPar time 3.52 Seconds 59.805 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-817-547A-17 (1-5) from US08817547A.pep 36 1 HNLGK 5

Scoring table: РАМ 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 17.545; Variance 13.620; scale 1.288

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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20 20 20 20 20 20 20 20	Result
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PARATHYROID HORMONE (F ORF CO4015. LIPOXYGENASE (FRAGMENT ER LUMENAL CHAPERONE B THREE ROWS PROTEIN. YWIA, SBO, YWIB, ARGS CC3 (CC3). HYPOTHETICAL 35.7 KD P RETINAL HOMEOBOX PROTE HYPOTHETICAL 38.6 KD P 60 KD CHAPERONIN (PROT ATP-DEPENDENT RNA HELI CONSERVED PROTEIN. RANSMISSION-BLOCKING T RHOPTRY PROTEIN (FRAGM RAT HEMOGLOBIN BETA-CH VPR PROTEIN (FRAGM VPR PROTEIN. ZERO BETA-1 GLOBIN. DBETA-2 GLOBIN.	Description
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POLYPROTEIN.	PLEXIN PRECURSOR.	HYPHAL GROWTH CHSE PRO	POLYPROTEIN (FRAGMENT)	RECEPTOR-ASSOCIATED TY	POLYMERASE.	GRLB.	FLOTILLIN.	POLYPROTEIN.	KIAA0187 PROTEIN.	HYPOTHETICAL 116.5 KD	PRECURSOR PEPTIDE.		PANCREATIC PEPTIDYLGLY	COMPLETE GENOME.	POLYMERASE.	P-PROTEIN.	DNA-DIRECTED DNA POLYM	ALDEHYDE FERREDOXIN OX	MEROZOITE SURFACE PROT	RHOPTRY ASSOCIATED PRO	COSMID TO7E3.	Ŧ	HYPOTHETICAL 29.2 KD P	PROTEIN 28 XII.
8.38e+01	8.38e+01	8.38e+01	8.38e+01	8.38e+01	8.38e+01	8.38e+01	8.38e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01

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ORE COMPUS. SULFOLOBUS SOLFATARICUS. ARCHAEBACTERIA; CRENARCHAEOTA; SULFOLOBALES. [1] SEQUENCE FROM N.A. SERAIN-P2; SERSEN C.W., KLENK H.P., SINGH R.K., ALLARD G., CHAN C.C.Y., LIU Q.Y., PENNY S.L., YOUNG F., SCHENK M.E., GAASTERLAND T., DOOLITTLE W.F., RAGAN M.A., CHARLEBOIS R.L.;	LT 2 P95954 P95954 P95954 P959554 O1-MAY-1997 (TREMBLREL. O3, CREATED) O1-MAY-1997 (TREMBLREL. O3, LAST SEQUENCE UPDATE) O1-MAY-1997 (TREMBLREL. O3, LAST ANNOTATION UPDATE) OBF COAOTS	Query Match 100.0%; Score 36; DB 10; Length 105; Best Local Similarity 100.0%; Pred. No. 5.59e+00; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 30 HNLGK 34	RATTUS NORVEGICUS (RAT).  EUTHARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  EUTHERIA; RODENTIA.  [1]  SEQUENCE FROM N.A.  11SSUBE-THYROID, AND PARATHYROID;  SCHMELZER H.J., GROSS G., MAYER H.;  ADV. GENE TECHNOL. 21:228-229(1984).  EMBL; M48475; 660193;  NON_TER  1 1  NON_TER  1 1  SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;	IT 1 Q63473 PRELIMINARY; PRT; 105 AA. Q63473; Q1-NOV-1996 (TREMBLREL. 01, CREATED) Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) PARATHYROID HORMONE (FRAGMENT).

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RL MOL. MICROBIOL. 22:175-191(1996).

DR EMBL, Y08257, E283828;

SO SEQUENCE 123 AA, 14021 WW; 316E0391 CRC32;

Query Match

Best Local Similarity 100.0%; Score 36; DB 9; Length 123;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 HNLGK 10

Qy 1 HNLGK 5

Search completed: Thu Jul 30 10:35:11 1998

Job time: 34 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:38:52 1998; MasPar time 2.75 Seconds 78.050 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-18 (1-14) from US08817547A.pep 103 1 LRKKLQDVHNFVAL 14

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Listing first 4.5 summaries

Database:

a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part5 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 19.363; Variance 67.336; scale 0.288

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

118544321 118544321 118544321	Result
	Score
111111111111111111111111111111111111111	Query Match L
33 33 33 33 33 33 33 33 33 33 33 33 33	Length DB
R58283 R58134 R58133 R58137 R58137 R58137 P30015 W21946 W21946 W21946 R23387 R23387 R231188 R211188 R211188 R211188 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R211286 R21286 R21286 R21286 R21286 R21286 R21286 R21286 R21286 R21286 R21286 R21286 R21286 R21286	Ħ
[Trp(Pmc)23]-hPTH(1-3) (Ser22]-hPTH(1-38)-OH [Ile19]-hPTH(1-38)-OH [Asp19]-hPTH(1-38)-OH [Asp19]-hPTH(1-38)-OH [Phe20]-hPTH(1-38)-OH Human parathyroid hor Porcine parathyroid hor Porcine parathyroid hor Human parathyroid hor Porcine Parathyroid hor Par	Description
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45	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	•
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P80275	R23449	R23313	R23344	R23326	R23299	R23394	R23275	R23402	R23290	R21168	R23258	R21227	R23439	R21192	R23237	R23378	R23241	R23415	R23317	W29420	R21240	R23441	R23265	R21222	116161
Sequence of human pre	Porcine parathyroid h		Bovine parathyroid ho		Bovine parathyroid ho		Bovine parathyroid ho	Porcine parathyroid h	Bovine parathyroid ho	Human parathyroid hor	Bovine parathyroid ho	Human parathyroid hor		Human parathyroid hor	Human parathyroid hor		Human parathyroid hor	Porcine parathyroid h	Bovine parathyroid ho	Human parathyroid hor	Human parathyroid hor	Porcine parathyroid h	Bovine parathyroid ho		
1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-0	1.80e-0	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	1.80e-03	F

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RESULT RE
                         PD 02-FED-1994.

PD 02-FED-1994.

PD 12-JUL-1993; GB-015009.

PR 15-JUL-1992; GB-026415.

PR 15-DEC-1992; GB-026851.

PR 23-DEC-1992; GB-026861.

PR 23-DEC-1992; GB-001691.

PR 28-JAN-1993; GB-001692.

PR 14-APR-1993; GB-001692.

PR 14-APR-1993; GB-008033.

PA (SANO) SANDOZ LID.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

PA (SANO) SANDOZ-ERFINDUNGEN VE
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hypoparathyroidism.
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38
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/note= "Trp(Pmc) where Pmc is
2,2,5,7,8-Pentamethylchroman-6-sulphonyl."
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Sequence

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Search completed: Thu Jul 30 10:39:16 1998 Job time: 24 secs.
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PF 12-JUL-1993; 014384.

PF 12-JUL-1993; 014384.

PR 15-JUL-1992; GB-015009.

PR 18-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026859.

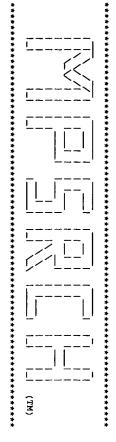
PR 23-DEC-1992; GB-026859.

PR 28-JAN-1993; GB-001691.

PR 14-APR-1993; GB-001691.

PR 16-APR-1993; GB-001692.

PR 16-APR-1993; GB-001
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Best Local Similarity 100.0%;
Matches 14; Conservative
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[Ser22]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
hypoparathyroidism.
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R58151 standard; peptide; 38
R58151;
                                                                                                                              24 lrkklqdvhnfval 37
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                                                                                                   1 LRKKLQDVHNEVAL 14
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                                                                                                                                                                                                  Score 103; DB 9; Le
Pred. No. 1.80e-03;
0; Mismatches 0;
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Pred. No. 1.80e-03;
0; Mismatches 0;
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:38:07 1998; MasPar time 3.41 Seconds 150.175 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-18
(1-14) from US08817547A.pep
103
1 LRKKLQDVHNFVAL 14

Scoring table:

Searched: PAM 150 Gap 15 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 26.838; Variance 43.748; scale 0.613

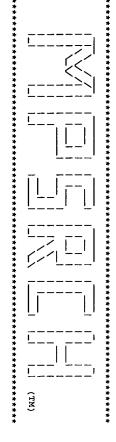
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 3 3 4 4 4 4 4 4 7 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ult No.
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53.4	•		٠	53.4		•		•	54.4	54.4	54.4	54.4	54.4	54.4	54.4		55.3	•			
1634	911	692	453	284	227	203	119	102	752	651	808	478	477	475	445	208	555	525	470	281	2845
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phosphoinositide 3-ki	ste6 protein - fissio	follitropin receptor	hypothetical protein	dimethyladenosine tra	prolactin-like protei	DNA-directed RNA poly	parathyroid hormone p	probable membrane pro	complement C2 precurs	DNA topoisomerase (EC	gag polyprotein - hum	<u>۔</u>	stromelysin 1 (EC 3.4	S	surface antigen - hep	RNAF		hypothetical protein	metalloelastase HME (	phosphoprotein phosph	adenomatous polyposis
4.33e+01	4.33e+01	4.33e+01	4.33e+01	4.33e+01	4.33e+01	4.33e+01	4.33e+01		3.06e+01		3.06e+01	3.06e+01	٠	3.06e+01	3.06e+01	3.06e+01		2.15e+01		2.15e+01	

RESULT 2  ENTRY  TITLE  parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic  ALTERNATE_NAMES n-succinyl-hpth(4-37) PDB_TITLE  ORGANISM  REFERENCE  # formal_name synthetic  # submission  submitted to the Brookhaven Protein Data Bank, June 1996 # cross-references PDB:12WG  REFERENCE  # authors  # submission  submitted to the Brookhaven Protein Data Bank, June 1996 # cross-references PDB:12WG  REFERENCE  # authors  # submission  Submitted to the Brookhaven Protein Data Bank, June 1996 # cross-references PDB:12WG  REFERENCE  # authors  # authors  IN 003319  # authors  # authors  IN 003319  # authors  # or authors  # or authors  # or authors  # or authors  # or authors  # o	Query Match 100.0%; Score 103; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 8.54e-08; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 21 LRKKLQDVHNFVAL 34 [	rs Resolu Determ	RESULT 1  INTERIOR   TITLE   parathyroid hormone (residues 4-37) - human    ALTERNATE_NAMES   HPTH(4-37)   structure of human parathyroid hormone fragment 4-37, NMR 10    STRUCTURES   A67860   STRUCTURES   ROSSCH, P.; MATX, U.C.   #submission   submitted to the Brookhaven Protein Data Bank, June 1996   #suchors   references PDB:12WE   REFERENCE   TUNO1721
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. on: Thu Jul 30 10:36:38 1998; MasPar time 2.28 Seconds 153.724 Million cell updates/sec

Title: Description: Perfect Score: Sequence: >US-08-817-547A-18 (1-14) from US08817547A.pep 103 1 LRKKLQDVHNFVAL 14

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 28.165; Variance 35.949; scale 0.783

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	3 : B
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b> 3	32	31	30	29	28	27	26	25	24
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POLG_PRSVH	KINH_NEUCR	HPR1_YEAST	FSHR_HORSE	FSHR_EQUAS	SYS_THETH	KAPO_HUMAN	KAPO_RAT	KAPO_BOVIN	KAPO_PIG	DP3E_BUCAP	YNOO_YEAST	Y17K_SSV1	FILS_HUMAN	UBA3_WHEAT	STE6_SCHPO	FSHR_CHICK	FSHR_RAT	KCC2_YEAST	HLYE_ECOLI	PRRA_RAT	RPOC_PROHO
GENOME POLYPROTEIN (CO	KINESIN HEAVY CHAIN.	HPR1 PROTEIN.	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	SERYL-TRNA SYNTHETASE	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	DNA POLYMERASE III, EP	21.	HYPOTHETICAL 17.8 KD P	FILENSIN (LENS FIBER C	UBIQUITIN-ACTIVATING E	STE6 PROTEIN.	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	CALCIUM/CALMODULIN-DEP	HEMOLYSIN E (HEMOLYSIN	PLACENTAL PROLACTIN-LI	DNA-DIRECTED RNA POLYM
1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.64e+01	1.08e+01	1.08e+01	1.08e+01	1.08e+01	1.08e+01	1.08e+01	1.08e+01	1.08e+01

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EIR. BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	PARATHYROID HORMONE PRECORSOR (PARATHYRIN) (PTH).	(REL. 3)	(REL. 01,	Ol, CREATED)	2	WIN SIANDAND,	TUV BOUTH STANDARD. DPT. 115		1 LRKKLQDVHNEVAL 14	55 lrkkiqdvhnfval 68	Query Match 100.0%; Score 103; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 1.98e-10; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	NCE 115 AA;	32 115 PA	26 31	1 25 BY		PROSITE; PS00335; PARATHYROID; 1.	EMBL; U15662; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION.	-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN		DEWILLE J.W., CAPEN C.C.;	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE; 95369696.	TISSUE=PARATHYROID;	SEQUENCE FROM N.A.	[1]			CANIS FAMILIARIS (DOG).		HORMONE PI	34,	(REL. 34,	2;	PTHY_CANFA STANDARD; PRT; 115 AA.	LT 1

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AD DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
LL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
C. -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
C. BONE AND PREVENTING THEIR RENAL EXCRETION.

REMBL; J00023; G163641; -.
EMBL; J00024; G163643; -.
EMBL; J00024; E18249; ALT_SEQ.
REMBL; J00024; E18250; ALT_INIT.
REMBL; M1938; G163647; -.
REMBL; M25082; G163645; -.
REMBL; M25082; G16364
                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 14; Conservative
                                                                                                                                                                              CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                     PROSITE;
HORMONE;
SIGNAL
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MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSO AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 26-115.

MEDLINE; 74142666.

HAMILYO, JW., NIALL H.D., JACOBS J.W., KEUTMANN COHN D.V.,

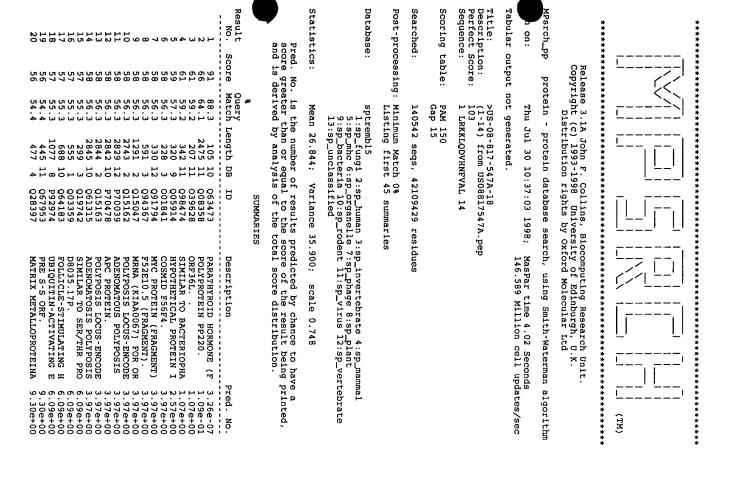
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656/107/1
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POTTS J.T. JR., TR
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MEDLINE; 71063634.

BREWER H.B. JR., RONAN R.;

PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEAVER C.A., GORDON D.F., GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHESIS OF 32-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 84262483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 80056617.
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55 LRKKLQDVHNEVAL
                                                                                                                                                                                                                                                                                          SIGNAL.
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32
106
115 AA;
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ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                         25
31
115
106
V
12980 MW;
    14
                                           89
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                                                                                  Score 103; DB 1; Le
Pred. No. 1.98e-10;
0; Mismatches 0;
                                                                                                                                                                         PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
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                                                                                                                              Length 115;
                                                                                       Indels
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                                                                                    Gaps
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Search completed: Thu Jul 30 10:36:46 1998 Job time: 8 secs.



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G., 93).	US (	01, 02,	ARY		3¢; 7¢; Ve	RATHYRO G., MAY 228-229 	) RDATA	01, 01, 05, RAGME	ARY;		111
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i.	71V) (ASFV). ; IRIDOVIRIDAE.	IED) SEQUENCE UPDATE) ANNOTATION UPDATE)	2475 AA.		l; DB 10; Length 105; 5. 3.26e-07; smatches 1; Indels 0;	63E CRC32;	BRATA; TETRAPODA; MAMMALIA;	ED) SEQUENCE UPDATE) ANNOTATION UPDATE)	105 AA.	S	COMPLEMENT COMPONENT C UBIQUIIN-ACTIVATING E CAM KINASE II (FRAGMEN PUTATIVE MADS-BOX FAMI AGLIS TYPE 2. DIMETHYLADENOSINE TRAN ALLERGEN (CR-PII). HYPOTHETICAL 50.0 KD P OVARIAN FOLLICLE-STIMU GLYCOGEN PHOSPHORYLASE ZINC FINGER PROTEIN (F ZINC FINGER PROTEIN (F ZINC FINGER PROTEIN (F RHOPTRY PROTEIN (FRAGM CHLOROQUINE RESISTANCE CHLOROQUINE RESISTANCE CHLOROQUINE RESISTANCE CHLOROQUINE RESISTANCE STRAIN HB3 CG2 (GG2). MACROPHAGE METALLOELAS K04G2.6. C06G3.9 PROTEIN. YFOTHETICAL 104.6 KD VINCULIN. PRSY YK POLYPROTEIN. CONNECTIN/TITIN (FRAGM
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RP COMPLETE GENOME.

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA CONDIGUEZ J.F., VINUELA E.;

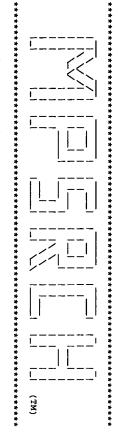
RA RODRIGUEZ G.F., VINUELA E.;

RA RODRIGUEZ J.F., VINUELA E.;

RA RODRIGUEZ J.F., VINUELA E.;

RA RODRIGUEZ L., ENRIQUEZ C.,

RA RODR
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. on: Thu Jul 30 10:41:57 1998; MasPar time 2.73 Seconds 73.134 Million cell updates/sec

Description: Perfect Score: Title: >US-08-817-547A-19 (1-13) from US08817547A.pep 95 1 RKKLQDVHNEVAL 13

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.828; Variance 67.821; scale 0.278

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

110 9 8 7 6 5 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
<b>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</b>	Score
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	Length DB
9 R51 9 R55 9 R55 9 R55 9 R55 27 W22 27 W22 27 W22 24 R R22 24 R R22 24 R R22 25 R R22 27 R R22 27 R R22 27 R R22	B ID
R58123 R580134 R580138 R581318 R58124 P300124 R721946 R7235607 R72335607 R72335607 R72335607 R72335607 R72335607	} } ! ! !
[Ser19]-hPTH(1-38)-OH [I1e19]-hPTH(1-38)-OH [I1e19]-hPTH(1-38)-OH [Phe20]-hPTH(1-38)-OH [Lys19]-hPTH(1-38)-OH [Lys19]-hPTH(1-38)-OH Human parathyroid hor Fusion protien compri Human parathyroid hor Porcine parathyroid hor Porcine parathyroid hor Porcine parathyroid hor Porcine parathyroid hor Human parathyroid hor Human parathyroid hor Porcine parathyroid hor	Description
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20-SEP-1994 (first entry)

DE [lle19]-hpHy[-18] off

KW

Human parathyroidism.

KW

Calcium; depletion, fixation; rescrption; osteopathy; osteoporosis;

KW

KW

Human parathyroidism.

KW

Calcium; depletion, fixation; rescrption; osteopathy; osteoporosis;

KW

KW

Calcium; depletion, fixation; rescrption; osteopathy; osteoporosis;

KW

Calcium; depletion, fixation; rescrption; osteopathy; osteoporosis;

KW

Calcium; depletion, fixation; rescrption; osteopathy; osteoporosis;

KW

CO2-FEB-1994.

KW

HUMAN postable

13-JUL-1922; GB-036415.

PR

12-JUL-1923; GB-036415.

PR

12-JUL-1923; GB-036415.

PR

12-JUL-1923; GB-036613.

28-JAN-1933; GB-001692.

28-JAN-1933; GB-001692.

28-JAN-1933; GB-001692.

28-JAN-1933; GB-001693.

28-JAN-1934; GB-001693.

28-JAN-1935; GB-001692.

PR

19-AR-1935; GB-001693.

PR

19-AR-1936; GB-001693.

PR

19-AR-1936; GB-001693.

PR

19-AR-1937; GB-001693.

PR

19-AR-1936; GB-001693.

PR

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PR

19-AR-1938; GB-001693.

PR

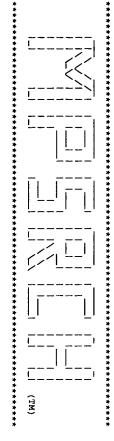
19-AR-1938; GB-001693.

PR

19-AR-1939; GB-001692.

PR

19-AR-193
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

92: Thu Jul 30 10:41:13 1998; MasPar time 3.44 Seconds 138.161 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-19 (1-13) from US08817547A.pep 95 1 RKKLQDVHNFVAL 13

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.919; Variance 39.318; scale 0.659

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

NO. 100 110 110 110 110 110 110 110 110 11	. Score 955 955 16	Query Matery 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Length 34 34 35 36 37 115 115 115 115 115 115 115 115	322112153555555 <u>D</u>	ID IZWE 12WG 1ZWF 1ZWF 1ZWH 1ZWB 1HPH 1ZWC 0704200 97180 97180 97180 97180 97180 97180 97180 97180 97180 97180	
108	5 0 0 0 0 0 0 0	100.0	115 115 115	- N P U	PTHU JC4202	
12	93		115 115	21	PTBO A05091	
13	83	87.4	105	Ν	I51851	roid
14 15	76 76	80.0		ທ ທ	1HTH 1ZWA	cyclic parathyroid parathyroid
16	5 8			N	S42547	7
17 18	58 57		2475 555	ผผ	S35307 S69641	polyprotein pp220 pr hypothetical protein
19	56	58.9	281	N	S41854	phosphoprotein phosph
20	56	•	444	Ν	S09681	citrate transport
21	56	•	475	jus	KCRTIH	stromelysin 1 (EC
22	56	•	477	_	KCMSS1	<u>-</u>
23	56		170	_		

45	44	43	42	41	40	39	38	37	36	<b>ω</b>	34	33	32	31	30	29	28	27	26	25	24
53	53	53	53	53	53	53	53	53	53	53	53	54	54	54	54	54	54	54	54	55	56
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S27337	S73824	S65947	JN0066	S20444	A43480	A46400	A49499	A42401	G64698	1ATO	S70651	JQ1899	PN0568	S51866	JC2237	A46312	C64313	S43492	S53076	A34548	G64068
multidrug resistance	MG242 homolog H91_orf	leukotriene-A4 hydrol	leukotriene-A4 hydrol	leukotriene-A4 hydrol	segmentation gene hed	segment polarity prot	metalloelastase HME (	macrophage elastase (	16S rRNA - Helicobact	17-hedgehog 17-kda fr	leukotriene-A4 hydrol	genome polyprotein -	connectin 3B - chicke	HPR1 protein - yeast	follitropin receptor,	gag polyprotein - hum	hypothetical protein	surface antigen – hep	probable membrane pro	follitropin receptor	DNA topoisomerase (EC
3.62e+0	3.62e+01	3.62e+0	3.62e+0:	3.62e+0:		2.50e+0	2.50e+01	2.50e+01	2.50e+01	2.50e+0:	2.50e+0	2.50e+0	1.71e+0	1.17e+0							

#book in F COMMENT Resolution	REFERENCE TNO #authors Mai	rs ssion -referen	ALTERNATE_NAMES n - S PDB_TITLE Suc ORGANISM #fc REFERENCE A67	,	Db 22 RKKLQDVHNEVAL	Query Match Best Local Similarity Matches 13; Conse	SUMMARY #1e	Resolu Determ	#authors Mar #book in	eferen	rs	ORGANISM #fc	NATE_NAMES	RESULT 1
in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable	TN003319 Marx, U.C.	Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 ces PDB:12MG	n-succinyl-nptn(4-3/) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic A67743	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic	VAL 34      VAL 13	100.0%; Score 95; DB 5; Length 34; Similarity 100.0%; Pred. No. 3.06e-07; 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR hormone			Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996	structures #formal_name Homo sapiens #common_name man a lack</td <td>parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10</td> <td></td>	parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10	

disease mutation; hormone; signal  #region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5  larity 100.0%; Score 95; DB 5; Length 34; Conservative 0; Mismatches 0; Indels
0; 5508
Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Psrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:39:34 1998; MasPar time 2.25 Seconds 145.141 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-19 (1-13) from USO8817547A.pep 95 1 RKKLQDVHNFVAL 13

Description: Perfect Score: Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 27.177; Variance 32.181; scale 0.844

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

sult	Score	Query Match	Length I	BB	ID	Description	Pred. No.
٦	95	100.0	115	ь ;	PTHY_CANFA	PARATHYROID HORMONE PR	8.93e-10
2	95	100.0	115	Н	PTHY_BOVIN	HORMONE	
ω	95	100.0	115	۲	PTHY_PIG	PARATHYROID HORMONE PR	
4	95	100.0	115	۳	PTHY_HUMAN	PARATHYROID HORMONE PR	
Сī	93	97.9	115	Н	PTHY_RAT	PARATHYROID HORMONE PR	.05e-
6	58	61.1	184	۳	GLG2_ARATH	GLUCOSE-1-PHOSPHATE AD	8.46e-01
7	56	٠	281	۲	P2C1_YEAST	PROTEIN PHOSPHATASE 2C	.186
<b>&amp;</b>	56	8	444	۲	CIT1_KLEPN	CITRATE-PROTON SYMPORT	2.18e+00
9	56	8	475	.,	COG3_RAT	STROMELYSIN-1 PRECURSO	2.18e+00
10	56		477	μ	COG3_MOUSE	STROMELYSIN-1 PRECURSO	2.18e+00
11	56	.8	478	μ	COG3_RABIT	STROMELYSIN-1 PRECURSO	2.18e+00
12	56	8	651	سر	TOP3_HAEIN	DNA TOPOISOMERASE III	2.18e+00
13	55	7.	692	بر	FSHR_RAT	FOLLICLE STIMULATING H	3.46e+00
14	55	7	693	μ	FSHR_CHICK	FOLLICLE STIMULATING H	3.46e+00
15	54	56.8	102	سر	YM88_YEAST	VERY HYPOTHETICAL 11.8	5.46e+00
16	54	σ.	130	۲	FILS_HUMAN	FILENSIN (LENS FIBER C	5.46e+00
17	54		525	۲	Y107_METJA	HYPOTHETICAL PROTEIN M	5.46e+00
18	54	5	687	<b>ب</b> سو	FSHR_EQUAS	FOLLICLE STIMULATING H	:
19	54		694	μ	FSHR_HORSE	FOLLICLE STIMULATING H	5.46e+00
20	54	σ.	752	۳	HPR1_YEAST	HPR1 PROTEIN.	5.46e+00
21	54	5	3344	μ	POLG_PRSVH	GENOME POLYPROTEIN (CO	5.46e+00
22	53	5	462	μ	COGM_MOUSE	MACROPHAGE METALLOELAS	8.55e+00
23	53	55.8	470	_	COGM_HUMAN	MACROPHAGE METALLOELAS	8.55e+00

<b>5</b>	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
50	51	51	51	51	51	51	51	51	51	52	52	52	52	52	<b>σ</b>	53	53	53	53	53	53
52.6	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	54.7	54.7	54.7	54.7	54.7	55.8	55.8	55.8	55.8	55.8	55.8	55.8
419	1444	1302	695	636	476	232	227	200	119	925	695	695	476	189	2133	1321	632	610	610	609	471
۳	Н	μ	Н	Н	Н	μ	Н	ш	Н	بر	ب	ш	Н	Н	۲	ш	_	_	_	سر	_
MYC1_XENLA	RRPL_RDV	RRPL_BTV10	FSHR_PIG	RPOC_CYAPA	COGX_HUMAN	RM16_YEAST	PRRA_RAT	YIGP_ECOLI	RT13_ACACA	DBL_HUMAN	FSHR_SHEEP	FSHR_BOVIN	COGX_RAT	YNOO_YEAST	FA8_PIG	MDR1_CAEEL	Y242_MYCPN	LKHA_MOUSE	LKHA_HUMAN	LKHA_RAT	HH_DROME
ONCOG	RNA-DIRECTED RNA POLYM	RNA-DIRECTED RNA POLYM	FOLLICLE STIMULATING H	DNA-DIRECTED RNA POLYM	STROMELYSIN-2 PRECURSO	PROBABLE MITOCHONDRIAL	PLACENTAL PROLACTIN-LI	HYPOTHETICAL 22.3 KD P	MITOCHONDRIAL RIBOSOMA	PROTO-ONCOGENE DBL PRE	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	STROMELYSIN-2 PRECURSO	VERY HYPOTHETICAL 21.7	COAGULATION FACTOR VII	MULTIDRUG RESISTANCE P	HYPOTHETICAL PROTEIN M	LEUKOTRIENE A-4 HYDROL	LEUKOTRIENE A-4 HYDROL	LEUKOTRIENE A-4 HYDROL	HEDGEHOG PROTEIN PRECU
3.16e+01	2.06e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	8.55e+00														

RES ACC DT	δ δ	CSS CSS Train CSS CSS Train CSS CSS Train CSS CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSS Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train CSs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Train Cs Tra Train Cs Trai Tra Train Cs Tra Train Cs Tra Tra Tra Tra Tra Tra Tra Tra Tra Tra	E D D C C R R R R R R R R R R R R R R R R	38885 5	B 3 3 3 5	RESULT ID P
RESULT 2  ID PTHY_BOVIN  AC P01268;  DT 21-JUL-1986  DT 21-JUL-1986  DT 01-NOV-1997  DRANTHYROID  DR PTH.  OS BOS TAURUS (  CC EUKARYOTA; M	Matches 13; Conse 56 RKKLQDVHNEVAL            1 RKKLQDVHNEVAL	AL EP ENCE atch cal S	SEQUENCE FROM N.A. TISSUE-PARATHYROID: MEDLINE: 9536966. ROSOL T.J., STEINMEYER ROSOL T.J., CAPEN C.GEMILLE J.W., CAPEN C.GEMILLE J.W., CAPEN C.GEMILLE J.W., CAPEN C.GEMILLE J.W., CAPEN C.GEME 160:241-243(1995) -1- FUNCTION: PTH ELEVY BONE AND PREVENTIN EMBL: U15662; G558916; PROSITE: PS00335; PARA! HORMONE: SIGNAL.	PTH.  CANIS FAMILIARIS (DC EUKARYOTA; METAZOA; EUTHERIA; CARNIVORA.  [1]	P52212; 01-0CT-1996 01-0CT-1996 01-0CT-1996 PARATHYROID	ULT 1 PTHY_CANFA
STANDARD;  (REL. 01, CREATED)  (REL. 01, LAST SEQ (REL. 35, LAST ANN HORMONE PRECURSOR (BOVINE).	rvative 68 13	25 31 115 12957 MV 100.0%; 100.0%;	SEQUENCE FROM N.A.  TISSUE-PARATHYROID;  TISSUE-PARATHYROID;  MEDLINE; 95369696.  MEDLINE; 95369696.  MEDLINE; 95369696.  MEDLINE; 953699696.  C.C.;  DEWILLE J.W., CAPEN C.C.;  DEWILLE J.W., CAPEN C.C.;  CENE 160:241-243(1995).  -1- FUNCTION: PTH ELEVATIES CALCIUM LEVEL  BONE AND PREVENTING THEIR RENAL EXCR  EMBL: U15662; G558916;  EMBL: U15662; G558916;  PROSITE; PS00335; PARATHYROID; 1.  HOMMONE: SIGNAL.	PTH. CAN'IS FAMILIARIS (DOG). EUKARYOTA; METAZOA; CHORDATA; EUTHERIA; CARNIVORA. [1]	(REL. 34, CREATED) (REL. 34, LAST SEC (REL. 34, LAST ANN HORMONE PRECURSOR	STANDARD;
ARD; PRT; 115 AA.  CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) PRECURSOR (PARATHYRIN) (PTH).  CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	0; Mismatches 0; Indels 0; Gaps 0;	BY SIMILARITY. BY SIMILARITY. 16EDOEBC CRC32; 10EDOEBC CRC32; 200re 95; DB 1; Length 115; 200re 95, DB 10; Trdels 0: Gang	MCCAULEY L.K., GRONE A., ALCIUM LEVEL BY DISSOLVING THE SALTS IN R RENAL EXCRETION. D; 1.	; VERTEBRATA; TETRAPODA; MAMMALIA;	(REL. 34, CREATED) (REL. 34, LAST SEQUENCE UPDATE) (REL. 34, LAST ANNOTATION UPDATE) HORMONE PRECURSOR (PARATHYRIN) (PTH).	PRT; 115 AA.

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DR DR DR DR DR FT FT ST
Q
                         밁
                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                                                           EMBL; V00106; G85; -.
EMBL; J00023; G163641; -.
EMBL; J00024; G163643; -.
EMBL; J00024; E18249; ALT_SEQ.
EMBL; J00024; E18250; ALT_INIT.
EMBL; K01938; G163647; -.
EMBL; M25082; G163645; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE; 82037785.

WEAVER C.A., GORDON D.F., KEMPER B.;

PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).

[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 80056617.

MEDLINE; 80056617.

MEDLINE; 80056617.

MATHANS J., SHARP P.A.,

METTS J.T. JR., RICH A.;

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 32-115.

MEDLINE; 71076162.

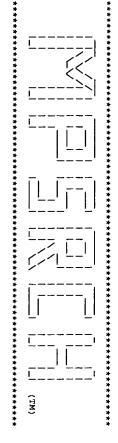
NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS AURBACH G.D., POTTS J.T. JR.;

HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANI
COHN D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA; ARTIODACTYLA.
[1]
                                                                                                  CHAIN
CONFLICT
SEQUENCE
                                                                                                                                     PROSITE;
HORMONE;
SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                               MEDLINE; 71091588.

POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D.,
DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE BONE AND PREVENTING THEIR RENAL EXCRETION.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 32-115.
MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [4]
                                                                                                                                                                                                                                                                                                                                                                         SYNTHESIS OF 32-65.
                         56
  دسو
                  RKKLQDVHNFVAL
                                                                                                                                                                                        A24949; A24949.
  RKKLQDVHNFVAL
                                                                                                                                                                SIGNAL.
                                                                                                                                                                           PS00335; PARATHYROID;
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26
32
106
115 /
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31
115
106
V
1080 MW;
   13
                           89
                                                                                                                                                                                                                                                                                                                                                                                                 R.;
U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KISSIL M.S., MEAD D.A., KEMPER B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JACOBS J.W., KEUTMANN
                                                  Score 95; DB 1; L
Pred. No. 8.93e-10;
0; Mismatches 0
                                                                                                   PARATHYROID HORMONE
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOGAN M.L., DAWSON B.F.,
                                                                            Length 115;
                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.T.,
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTTS J.T. JR.,
                                                                                                                                                                                                                                                                                                                THE SALTS
                                                                                                                                                                                                                                                                                                                                                    SAUER R.,
                                                       0
                                                       Gaps
                                                         0
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Search completed: Thu Jul 30 10:39:40 1998 Job time: 6 secs.



MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:39:58 1998; MasPar time 3.95 Seconds 138.577 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-817-547A-19 (1-13) from US08817547A.pep 95

Title:

Sequence: RKKLQDVHNFVAL 13

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 25.965; Variance 32.081; scale 0.809

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query Match	Length	BB	Ħ	Description	Pred. No.
ב	83	87.4	105	10	Q63473	PARATHYROID HORMONE (F	1.95e-06
2	13	4	207	11	039628	ORF36L.	2.58e-01
ω	60	63.2	342	11	Q98474	SIMILAR TO BACTERIOPHA	4.21e-01
4	58	61.1	2475	11	Q08358	POLYPROTEIN PP220.	1.10e+00
ر ت	57	60.0	555	ᆫ	Q03359	D8035.17P.	1.77e+00
σ	57	60.0	889	10	Q64183	FOLLICLE-STIMULATING H	1.77e+00
7	56	58.9	477	4	028397	MATRIX METALLOPROTEINA	2.82e+00
8	55		693	12	Q90719	OVARIAN FOLLICLE-STIMU	4.48e+00
9	55		1459	w	Q21874	R09E10.5.	4.48e+00
10	54		445	11	Q67953	PRE S-S ORF.	7.06e+00
11	54		993	ω	Q17162	VINCULIN.	7.06e+00
12	U1 4		1002	11	Q85025	HC, P3 AND CI PROTEINS	7.06e+00
13	54		1323	12	Q08476	CONNECTIN (TITIN) (FRA	7.06e+00
14	54		3344	11	P90213	PRSV YK POLYPROTEIN.	7.06e+00
15	54		4162	12	Q98918	CONNECTIN/TITIN (FRAGM	7.06e+00
16	53		269	w	Q19322	COSMID F10G7.	1.11e+01
17	53		271	9	025972	16S RRNA (ADENOSINE-N6	1.11e+01
18	53		299	w	Q19742	SIMILAR TO SER/THR PRO	1.11e+01
19	53	55.8	709	ω	015783	HYBRID HISTIDINE KINAS	1.11e+01
20	53		1321	w	Q21349	K08E7.9.	1.11e+01

45	44	43	42	41	40	39	38	37	36	<u>ω</u>	34	33	32	31	30	29	28	27	26	25	24	23	22	7.7
50	50	50	50	50	50	50	51	51	51	51	51	51	51	51	51	51	51	51	52	52	52	52	52	ŭ
	•	•	•	52.6	•	٠		53.7		53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7		54.7			54.7	•	•
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P70039	Q9885 <b>7</b>	042479	033405	Q91794	Q25942	Q25927	Q15058	Q98631	Q65740	Q65739	Q65741	Q65734	Q18824	Q66658	Q24250	Q94367	Q05914	Q07216	Q46606	P77171	P95793	Q42657	005658	023669
ADENOMATOUS POLYPOSIS	STROMELYSIN-1/2-A.	FERROCHELATASE (EC 4.9	HYDROGENASE SMALL SUBU	MYC PROTEIN (FRAGMENT)	MAJOR MEROZOITE SURFAC	MAJOR MEROZOITE SURFAC	MRNA (KIAA0042) FOR OR	RNA-DEPENDENT RNA POLY	RNA-DIRECTED RNA POLYM	RNA-DIRECTED RNA POLYM	RNA-DIRECTED RNA POLYM	CORE PROTEIN.	SIMILAR TO MULTIDRUG-R	DNA HELICASE-PRIMASE C	TARTAN PROTEIN PRECURS	F52E10.5 (FRAGMENT).	HYPOTHETICAL PROTEIN I	URA7 CTP SYNTHETASE.	HYD GAMMA.	FROM BASES 1485094 TO	STBA.	ANNEXIN.	LYSR-TYPE BETA-LACTAMA	2K930.1.
4.10e+01	4.10e+01	4.10e+01	4.10e+01		4.10e+01	4.10e+01		2.67e+01	2.67e+01	2.67e+01	2.67e+01	2.67e+01	2.67e+01	•	•		2.67e+01	2.67e+01	1.72e+01	1.72e+01	1.72e+01	1.72e+01	1.72e+01	1.11e+01

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RESULT COMMENTS OF THE PROPERTY OF THE PROPERT
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Matches
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039628
039628
079628
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079628
089628
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OT 1

PRELIMINARY; PRT; 105 AA.

063473;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
SEQUENCE FROM N.A.
JEHLE J.A., VAN DER LINDEN I.F.A.,
VIRUS RES. 0:0-0(1997).
EMBL, AF002732; G2233189; -.
SEQUENCE 207 AA; 23915 MW; D2F0
                                                                                                                                                                                                                                                                                                                                                ORF36L.
CYDIA POMONELLA GRANULOVIRUS.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-THYROID, AND PARATHYROID; SCHMELZER H.J., GROSS G., MAYER H.; ADV. GENE TECHNOL. 21:228-229(1984). EMBL; M54875; G601933; -. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARATHYROID HORMONE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 RKKLQDGHNFVSL 58
|||||| ||||:|
1 RKKLQDVHNFVAL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 87.4%;
Local Similarity 84.6%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 AA; 11746 MW; 6AC3163E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 83; DB 10;
Pred. No. 1.95e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
            D2F0E988 CRC32;
                                                                                                                                                                                       VLAK J.M.;
                                                                                                                                                                                                                                                                                                                                                            BACULOVIRIDAE; GRANULOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Query Match
Best Local Similarity 66.7%; Pred No. 2.58e-0);
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 144 RIOEVHDFV 152

Qy 3 KIODVHEV 11

Search completed: Thu Jul 30 10:40:55 1998

Job time: 57 secs.
```

Title: Description: Perfect Score: Sequence:	Mpsrch_pp protein - protein on: Thu Jul 30 : Tabular output not generated	**************************************	***
>US-08-817-547A-20 (1-12) from US08817547A.pep 86 1 KKLQDVHNFVAL 12	<pre>protein - protein database search, using Smith-Waterman algorithm     Thu Jul 30 10:44:34 1998; MasPar time 2.69 Seconds     68.390 Million cell updates/sec ut not generated.</pre>	**************************************	**************************************

Scoring table: PAM 150 Gap 15

124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.088; Variance 63.020; scale 0.287

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

17 18 19	115113	10 11 12	876U	4004	Result No.
0 0 0 0 0 0	, , , , , , , , ,	& & & & & & & & & & & & & & & & & & &	& & & & & & & & & & & & & & & & & & &	8888	Score
100.0	100.0	100.0	100.0	100.0	Query Match
8888	8888	8888	88888	38 9 44 26 47 25 84 27	Length DB
R21156 R21185	R23259 R23436 R23512	R23316 R23346 R23336		R58024 P30015 W21946 W25687	B ID
Human parathyroid I Human parathyroid I Human parathyroid I	Bovine parathyroid le porcine parathyroid le Bovine parathyroid le	Bovine parathyroid Bovine parathyroid Bovine parathyroid Porcine parathyroid	Bovine parathyroid Porcine parathyroid Porcine parathyroid Bovine parathyroid	[Ala1,Ile2]-hPTH(1-38 Human parathyroid hor Fusion protien compri Human parathyroid hor	Description
hor 6.03e-02 hor 6.03e-02 hor 6.03e-02	विच वि	ho 6.03e-02 ho 6.03e-02 ho 6.03e-02 d h 6.03e-02		38 6.03e-02 hor 6.03e-02 hor 6.03e-02 hor 6.03e-02	Pred. No.

В

26 kklqdvhnfval 37

86 100.0 84 4 R23370 Bovine parathyroid hor 86 100.0 84 4 R23169 Human parathyroid hor 86 100.0 84 4 R21169 Human parathyroid hor 86 100.0 84 4 R21170 Human parathyroid hor 86 100.0 84 4 R21230 Human parathyroid hor 86 100.0 84 4 R21231 Human parathyroid hor 86 100.0 84 4 R21212 Human parathyroid hor 86 100.0 84 4 R23395 Porcine parathyroid hor 86 100.0 84 4 R23189 Human parathyroid hor 86 100.0 84 4 R21189 Human parathyroid hor 86 100.0 84 4 R21189 Human parathyroid hor 86 100.0 84 4 R21165 Human parathyroid hor 86 100.0 84 4 R23164 Human parathyroid hor 86 100.0 84 4 R23168 Bovine parathyroid hor 86 100.0 84 4 R23169 Bovine parathyroid hor 86 100.0 84 4 R23169 Bovine parathyroid hor 86 100.0 84 4 R23258 Bovine parathyroid hor 86 100.0 84 4 R23259 Bovine parathyroid hor 86 100.0 84 4 R23290 Bovine parathyroid hor 86 100.0 84 4 R23290 Bovine parathyroid hor 86 100.0 84 4 R23298 Bovine parathyroid hor 86 100.0 84 4 R23208 Bovine para	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	0
0 84 4 R23370 0 84 4 R23370 0 84 4 R23169 0 84 4 R21169 0 84 4 R21169 0 84 4 R21170 0 84 4 R21170 0 84 4 R21170 0 84 4 R21230 0 84 4 R21231 0 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	86	ď
4 R23370  4 R23370  4 R23170  4 R23170  4 R21169  4 Human parathyroid  4 R21169  4 Human parathyroid  4 R211230  4 Human parathyroid  4 R21231  4 Human parathyroid  4 R21231  4 Human parathyroid  4 R21213  4 Human parathyroid  4 R21212  4 Human parathyroid  4 R23395  Bovine parathyroid  4 R21188  Human parathyroid  4 R21188  Human parathyroid  4 R21165  Human parathyroid  4 R21164  Human parathyroid  4 R21165  Human parathyroid  4 R21168  Human parathyroid  4 R23278  Bovine parathyroid  4 R23290  Bovine parathyroid  4 R23290  Bovine parathyroid  4 R23394  Human parathyroid  4 R23394  Forcine parathyroid  4 R23394  Forcine parathyroid  4 R23394  Human parathyroid  4 R23394  Bovine parathyroid  4 R23394  Human parathyroid  4 R23394  Forcine parathyroid  4 R23396  Forcine parathyroid		•		•	•	•					•												•		٠	٠
R23370  R23370  R23370  R23370  R23370  R23169  R231169  R231170  R231230  R231231  R231231  R231231  R231231  R231231  R231231  R231232  R231232  R231232  R231233  R231233  R231233  R231234  R231235  R231283  R231283  R231189	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	04
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ovine parathyroid uman parathyroid orcine parathyroid orcine parathyroid uman parathyroid uman parathyroid uman parathyroid uman parathyroid uman parathyroid uman parathyroid ovine parathyroid ovine parathyroid orcine parathyroid	R23449	R42069	R42067	R23904	R21208	R23394	R23275	R23402	R23290	R21168	R23258	R21164	R21165	R21189	R21188	œ	R23395	R21212	R21213	R21231	R21230	~	σ	N	337	C.
	orcine	tability-enhanced	parathyroid	parathyroid	parathyroid	Porcine parathyroid h	parathyroid	Porcine parathyroid h	parathyroid	parathyros	parathyroid	parachyroid														

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RESULT TO RESULT
Query Match
Best Local s
Matches 1
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D2-FEB-1993; 014384.

F 12-JUL-1993; GB-015009.

F 18-DEC-1992; GB-026415.

R 18-DEC-1992; GB-026859.

R 23-DEC-1992; GB-026859.

R 23-DEC-1992; GB-026861.

R 28-JAN-1993; GB-001692.

R 28-JAN-1993; GB-001692.

R 28-JAN-1993; GB-001693.

R 14-APR-1993; GB-007673.

R 19-APR-1993; GB-008033.

R 19-APR-1993; GB-0080833.

R 19-APR-1993; GB-008033.

R 19-APR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R58024 standard; peptide; 38 AA. R58024; 20-SEP-1994 (first entry) [Ala1,Ile2]-hPTH(1-38)-OH. Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism. Synthetic.
                                                                                                                                                                                                                      New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 10; Page 35; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism.

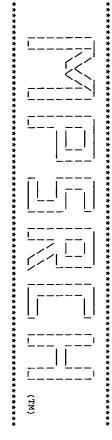
Sequence 38 AA;
h 100.0%;
Similarity 100.0%;
12; Conservative
Score 86; DB 9; L
Pred. No. 6.03e-02;
0; Mismatches 0
           0;
                                                                                                             Length 38;
           Indels
           0
           Gaps
           0
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δÃ

1 KKLQDVHNFVAL 12

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ID P30015 standard; peptide; 44 AA.
AC P30015,
AC P30015,
AC P30015
T1 11-SEP-1992 (first entry)
DE Human parathyroid hormone (1-44).

KW HPH; condensation; azide; active ester; carbodiimide.
OS Synthetic.
PN J57192350-A.
PD 25-APR-1991; 059750.
PR (AJIN) TANARAUSHITSU KENKY.
PR 22-APR-1991; JF-059750.
PR (AJIN) TANARAUSHITSU KENKY.
PR Peptide fragment (1-44) of human parathyroid hormone - prepd. by
Condensn. of individual amino acids or peptide fragments and
removing protecting gps. from condensed peptide
Claim i; Page 1: I/Pp; Japanese
Claim i; Page 1: I/Pp; Japanes
```



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:43:49 1998; MasPar time 3.30 Seconds 132.749 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-20 (1-12) from US08817547A.pep 86 1 KKLQDVHNFVAL 12

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.131; Variance 37.196; scale 0.676

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

11 11 12 13 13 14 14 15 16 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18	ult No.
\$\$\$\$\$\$\$\$\$\$\$\$\$\$\\\\\\\\\\\\\\\\\\\\\\\\	Score
100 0 100 0	% Query Match
34 34 35 36 37 37 37 31 37 31 37 37 37 37 37 37 37 37 37 37 37 37 37	Length
88884488488488488488	DB
12WE 12WE 12WF 12WF 12WF 12WD 12WD 12WC PTHU PTHU PTBO PTBO PTBO PTBO PTBO PTBO PTBO PTBO	IB
parathyroid hormone ( parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone ( parathyroid hormone ocyclic parathyroid hormone ( parathyroid hormone parathyroid hormone ( parathyroid hormone parathyroid hormone ( parathyroid hormone parathyroid hormone parathyroid hormone ( parathyroid hormone parathyroid ho	Description
7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 7.55e-06 6.21e-00 6.21e-00 6.21e-00 6.21e-00 9.26e-00	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	4
51	51	51	51	51	51	52	52	52	52	52	53	53	53	53	53	53	53	53	53	54	4
59.3	59.3	59.3	59.3	59.3	59.3	60.5	60.5	60.5	60.5	60.5	61.6	61.6	61.6	61.6	61.6	61.6				62.8	
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RNA-directed RNA poly	transforming protein	stromelysin 2 (EC 3.4	ribosomal protein L16	DNA-directed RNA poly	hypothetical 22.3 kD	follicle stimulating	follitropin receptor	hydrogenase homolog,	stromelysin 2 (EC 3.4	annexin - pepper	multidrug resistance	MG242 homolog H91_orf	leukotriene-A4 hydrol	leukotriene-A4 hydrol	leukotriene-A4 hydrol	segmentation gene hed	segment polarity prot	17-hedgehog 17-kda fr	leukotriene-A4 hydrol	genome polyprotein -	כטווופכינדוו טף - כוודכאפ
4.36e+01	4.36e+01	4.36e+01	4.36e+01	4.36e+01	4.36e+01	2.98e+01	2.98e+01	2.98e+01	2.98e+01	2.98e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	1.37e+01	F. U / G + C E

rs Rosein, P.; Marx, U.C. ssion submitted to the Brookhaven Protein Data Bank, June -references PDB:12WG     TN003319 rs Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in     pp.0, Bayreuth: University of Bayreuth (Thesis), Resolution: not applicable	IZWG #type complete  PATRY parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -  ALTERNATE_NAMES n-succinyl-hpth(4-37)  PDB_TITLE succinyl human parathyroid hormone 4-37, NMR, 10 structures  ORGANISM #formal_name synthetic  REFERENCE A67743	23 1	Query Match 100.0%; Score 86; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 7.55e-06; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps	15-25 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4128 #checksum 5508	#authors Marx, U.C.  #book in Strukturen Verschiedener Parathormonfragmente in Loes  pp.0, Bayreuth: University of Bayreuth (Thesis), 1996  COMMENT Resolution: not applicable  COMMENT Determination: NMR  KEYWORDS hormone	E A67860  Ors Roesch, P.; Marx, U.C. Ission submitted to the Brookhaven Protein Daviserences PDB:1ZWE E TN001721	type complete hormone (residues 4-37) - human human parathyroid hormone fragment 4-37,
1996 Loesung, 1996	D -		0,		Loesung, 1996	96	NMR 10

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COMMENT
EXAMPLES

Alsease mutation; hormone; signal
FENATURE

Logical March helix (right hand alpha)

STRMARY

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Query Match
Best Local Similarity 100.0%; Prod 86; DB 5; Length 34;

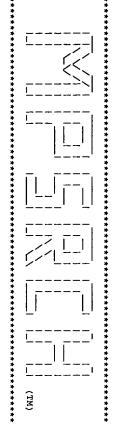
Matches 12; Conservative 0, Mismatches 0, Indels 0; Gaps 0;

Db 13 KYLOPHNEYAL 14

Oy 1 KYLOPHNEYAL 12

Search completed; Thu Jul 30 10:44:16 1998

Do time: 27 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:42:38 1998; MasPar time 2.23 Seconds 134.872 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A.pep
Perfect Score: 86

Sequence: 1 KKLQDVHNFVAL 12

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 26.327; Variance 30.652; scale 0.859

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11 12 13 14 14 14 15 16 17 17 17 17 17 17 17 17 17 17 17 17 17	NO.
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Best Local Similarity 100.0%;
Matches 12; Conservative
PARATHYROID HORMONE PI
PTH.
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; C
                                                                                                              PTHY_BOVIN
P01268;
21-JUL-1986
21-JUL-1986
01-NOV-1997
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P52212;
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01-0CT-1996
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CHAIN
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EMBL; U15662; G558916; -

PROSITE; PS00335; PARATHYROID; 1.
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TISSUS-PARATHYROID;
MEDLINE; 95369696.
ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K.,
DEWILLE J.W., CAPEN C.C.;
GENE 150:241-243(1995).
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CANIS FAMILIARIS (DOG).
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1 KKLQDVHNFVAL 12
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32
115 AA;
                                                                                  (REL. 01, CREATED)
(REL. 01, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
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(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                             STANDARD;
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31 BS
115 PI
12957 MW;
        CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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BY SIMILARITY.
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Pred. No. 5.76e-08;
0; Mismatches (
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Search completed: Thu Jul 30 10:42:44 1998 Job time : 6 Secs.

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PARATHYROID HORMONE (F 2.00e-04 0RF36L	cted by chance to have a of the result being printe score distribution.	sp_invertebrate 4:sp_mammal 7:sp_phage 8:sp_plant nt 11:sp_virus 12:sp_vertebrate 683; scale 0.791	G	puting Research Unit. of Edinburgh, U.K. of Molecular Ltd using Smith-Waterman algorith using time 3.89 Seconds 9.795 Million cell updates/sec	(ME)

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207 AA. ) QUENCE UPDATE) NOTATION UPDATE) E; BACULOVIRIDAE; GRANULOVIRUS VIAK J.M.; E988 CRC32;	4; DB 10; Length 105; io. 2.00e-04; smatches 1; Indels 0;	SEQUENCE UPDATE) ANNOTATION UPDATE)  RTEBRATA; TETRAPODA; MAMMALIA;  84.;  94).	TS 105 AA.	SIMILAR TO MULTIDRUG-R 1. RNA-DEPENDENT RNA POLY 1. RNA-DEPENDENT RNA POLY 1. RNA-DEPENDENT RNA POLY 1. RNA-DEPENDENT RNA POLY 1. RAYLALKYLAMINE N-ACETY 2. MAJOR MEROZOITE SURFAC 2. MAJOR MA
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Query Match 70.9%; Score 61; DB 11; Length 207; Best Local Similarity 66.7%; Pred. No. 1.70e-01; Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0; Db 144 RLQEVHDFV 152 :||:||:|| Qy 2 KLQDVHNFV 10

Search completed: Thu Jul 30 10:43:30 1998
Job time : 29 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Jul 30 10:47:12 1998; MasPar time 2.77 Seconds 60.925 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: Title: >US-08-817-547A-21 (1-11) from US08817547A.pep 79

Sequence: 1 KLQDVHNFVAL 11

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match Listing first 40 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Mean 17.545; Variance 61.494; scale 0.285

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

110 110 110 110 110 110 110 110 110 110	Result No.
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11111111111111111111111111111111111111	Query Match I
C C C C C C C C C C C C C C C C C C C	Length DB
R11882 R580224 R580224 R58123 R581152 R581152 R581159 R581159 R581159 R581159 R581159 R581159 R581159 R581159 R581159 R581159 R581159 R581159 R581159 R581159	Ħ
Parathyroid hormone f [Ala], I1e2]-hPTH(1-38)-OH [Ser19]-hPTH(1-38)-OH [Lys19]-hPTH(1-38)-OH [I1e22]-hPTH(1-38)-OH [Arg22]-hPTH(1-38)-OH [Arg22]-hPTH(1-38)-OH [Arg22]-hPTH(1-38)-OH [Ala]]-hPTH(1-38)-OH [Ala]]-hPTH(1-38)	Description
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P40251	P80306	R23449	R42074	R42068	R21169	R21170	R21241	R23425	R21168	R23258	R21189	R21188	R21183	R21238	R21212	R21213	R23327	R23549	W29420	R23483	R21156	R21257	R23485	R23259	R23429
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DE3935738-A.
08-MAY-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wpI; 91-141042/20.

New parathyroid hormone fragment and its naturally occurring derivs: - used to treat osteoporosis, hypertonia, hypoparathyroidism, electrolyte imbalance associated with kidney failure, etc.

Claim 1; page 6; 22pp; German.

This parathyroid hormone fragment, comprising residues 1-37, and its derivs. are useful for treating parathyroid gland disorders, degenerative bone disease, circulatory disease, lung disease, etc. Antibodies raised against the fragment are useful for diagnosing these diseases. The fragment and derivs. are administered as a lyophilisate with mannitol.

Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R11882 standard; protein; 37 AA.
R11882;
24-JUL-1991 (first entry)
Parathyroid hormone fragment (1-37).
Parathyroid hormone; osteoporosis; hypertonia; hypoparathyroidism; kidney failure; hypertension; acute renal insufficiency.
                                   R58024 standard; peptide;
R58024;
20-SEP-1994 (first entry)
[Ala1,Ile2]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-1989; 935738.
27-OCT-1989; DE-935738.
(FORS/) FORSSMANN W.
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Similarity 100.0%;
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Pred. No. 2.64e-01;
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££&3333338
                                                                                                                                                                                                                                  KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis; Synthetic.

Synthetic.

PM GB2269176-A.

PD 12-JUL-1993; 014384.

PF 12-JUL-1993; 014384.

PF 12-JUL-1993; 03-015009.

PR 15-JUL-1993; GB-026415.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026859.

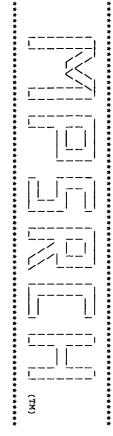
PR 23-DEC-1992; GB-026851.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-192; GB-026859.

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|||||||||
1 KLQDVHNFVAL 11
                                                                                                             Score 79; DB 9; Length 38; Pred. No. 2.64e-01; 0; Mismatches 0; Indels
                                                                                                             0;
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Qy Search completed: Thu Jul 30 10:47:36 1998 Job time: 24 secs. Вþ Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. on: Thu Jul 30 10:46:26 1998; MasPar time 3.26 Seconds 123.145 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-817-547A-21 (1-11) from US08817547A.pep 79 1 KLQDVHNFVAL 11

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 24.418; Variance 35.126; scale 0.695

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

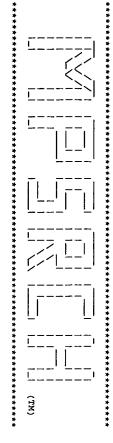
# SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	տ	4	ω	N	<b>J</b> 1	sult No.
50	51	51	51	52	53	53	53	60	60	67	77	79	79	79	79	79	79	79	79	79	79	79	Score
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217	1444	232	201	606	1321	632	555	34	34	105	115	115	115	115	115	37	37	36	35	34	34	34	Length
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	73	ribosomal protein L16	hypothetical 22.3 kD	hydrogenase homolog,	multidrug resistance	MG242 homolog H91_orf	hypothetical protein		đ	hormone	hormone	hormone	parathyroid hormone p	_	_	parathyroid hormone (	parathyroid hormone f	_	parathyroid hormone (	_	parathyroid hormone 4	parathyroid hormone (	Description
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JC4172	S22610	JC5145	S50054	G64068	KCRBS1	KCMSS1	KCRTIH	A43480	A46400	A26081	S07569	1ATO	B40535	PN0568	D36892	S28491	S40449	S25128	H40781	A49499	A42401
DNA (cytosine-5-)-met	DNA (cytosine-5-)-met	DNA (cytosine-5-)-met	chloride channel prot	DNA topoisomerase (EC	stromelysin 1 (EC 3.4	stromelysin 1 (EC 3.4	stromelysin 1 (EC 3.4	ation gene	segment polarity prot	epoxide hydrolase (EC	protein H5 - slime mo	17-hedgehog 17-kda fr	clathrin-associated p	connectin 3B - chicke	' -regic	hypothetical protein	pro-hormone convertas	<ul> <li>Autog</li> </ul>	hypothetical 60.7K pr	metalloelastase HME (	macrophage elastase (
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Search completed: Thu Jul 30 10:46:54 1998 Job time : 28 secs.	COMMENT KEYWORDS disease mutation; hormone; signal FEATURE 1-9 15-25 SUMMARY #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4128 #checksum 5508 Query Match Best Local Similarity 100.0%; Score 79; DB 5; Length 34; Matches 11; Conservative 0; Mismatches 0; Indels 0; Db 24 KLQDVHNFVAL 14 Qy 1 KLQDVHNFVAL 11
	Gaps
	0,



Psrch_pp on: protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 10:45:13 1998; MasPar time 2.26 Seconds 122.035 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-817-547A-21 (1-11) from US08817547A.pep 79 1 KLQDVHNFVAL 11

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 25.575; Variance 28.974; scale 0.883

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2222223	sult No.
44444444444444444444444444444444444444	Score
100.0 100.0 100.0 67.5 67.1 67.1 64.6 64.6 63.3 63.3 63.3 63.3 63.3 63.3	% Query Match
115 115 115 115 115 632 1321 1321 1444 462 470 470 831 1142 1142 475 477 477 477 477	Length
	BB
PTHY_CANFA PTHY_BOVIN PTHY_BIG PTHY_HUMAN PTHY_RAT Y242_MYCPN MDRI_CAEEL Y1GP_ECOLI RM16_YEAST RPL_RDV COGM_MOUSE COGM_RAT HYEP_RAT HYEP_RAT HYEP_RAT HYEP_RAT HYEP_RAT COGM_RAT COGM_RAT COGM_RAT COGM_RAT COGM_ROUSE COGM_RAT COGM_ROUSE COGM_RAT	SUMMARIES
DDDDARAHE BOOO DRYNO	Description
1.01e-06 1.01e-06 1.01e-06 1.01e-06 2.15e-00 2.15e+00 2.15e+00 5.64e+00 5.64e+00 9.04e+00 9.04e+00 9.04e+01 1.44e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
47	47	47	47	47	48	48	48	48	<b>4</b> 8	48	48	48	48	48	48	48	48	48	48	49	49
•		•	•		60.8	•	•	•	•	60.8	•	•	•	٠	•	60.8	60.8	•	•	•	62.0
3344	694	687	649	274	4725	1620	1318	933	881	827	693	692	410	409	398	328	317	153	136	1495	779
Н	_	ب	ب	ட	Н	Ь	μ	Ь	ш	Ь	Ь	Ъ	μ	۲	μ	μ	سر	ш	ب	Н	Н
POLG_PRSVH	FSHR_HORSE	FSHR_EQUAS	FAF1_MOUSE	CD1_SYLFL	DYHC_DICDI	MIDM_MOUSE	VIVD_BPT7	CC54_YEAST	HELI_VZVD	RED1_YEAST	FSHR_CHICK	FSHR_RAT	NADR_ECOLI	NADR_SALTY	YQFD_BACSU	LDH_STRMU	YG00_HAEIN	ML11_BRARE	Y441_MYCPN	MTDM_HUMAN	GEF1_YEAST
GENOME POLYPROTEIN (CO	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	FAF1 PROTEIN (FAS-ASSO	T-CELL SURFACE GLYCOPR	DYNEIN HEAVY CHAIN, CY	DNA (CYTOSINE-5)-METHY	INTERNAL VIRION PROTEI	CELL DIVISION CONTROL	PROBABLE HELICASE.	RED1 PROTEIN.	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	TRANSCRIPTIONAL REGULA	GGF	HYPOTHETICAL 45.7 KD P	L-LACTATE DEHYDROGENAS	HYPOTHETICAL PROTEIN H	MELATONIN RECEPTOR TYP	HYPOTHETICAL PROTEIN M	DNA (CYTOSINE-5)-METHY	GEF1 PROTEIN (VOLTAGE-
•	3.55e+01		3.55e+01	3.55e+01	2.27e+01	2.27e+01	2.27e+01			2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01		2.27e+01		1.44e+01	1.44e+01

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BOS TAURUS (		DARATHVROTO	01 - NOV - 1997	21-JUL-1986	21-JUL-1986	P01268;	L'HY BOY IN	,			1 KLQDVHNEVAL		58 KIODVHNEVAL	Matches 11;	Best Local Simi	erv Match	NCE	CHAIN	PROPEP			PROSITE; PS	EMBL; U1566;		-!- FUNCTION	GENE 160:241	DEWILLE J.W	ROSOL T.J.,	MEDLINE; 95369696.	TISSUE-PARATHYROID;	SEQUENCE FROM N.A.	[1]	EUTHERIA: CARNIVORA	CANIS FAMIL		PARATHYROID	01-OCT-1996	01-OCT-1996	01-OCT-1996		PTHY CANFA	LT 1
(BOVINE). METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		HORMONE DR	(REL 35 LAST ANNOTATIO	(REL. 01,	(REL.		STANDARD; FRT; 113 AA.				HNEVAL 11		HNEVAL 68	11; Conservative 0; Mismatches 0; Indels 0; Gaps	100.0%; Pred. No. 1.01e-06;	Score 79: DB 1:	AA; 12957 MW;	7	31	25 BY			; G558916;	G THEIR RENAL EXCRETION.	FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN	GENE 160:241-243(1995).		ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	5369696.	ATHYROID;	ROM N.A.	CHAIL FORD.	METAZOA; CHORDATA; VERTEBRATA; TETRAFODA; MAMMALIA; CARNIVORA	OG).		HORMONE PRECUR	(REL. 34, LAST	(REL. 34,	(REL.		STANDARD; PRT; 115 AA.	
														0;																												

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                                                                                                                                                                                                                                                                                                                MEDLINE; 71091588.

A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

A DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

PROC. PROC. PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SCHOOL DAY OF THE SCHOOL OF TH
                                                                                   Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS POTTS J.T. JR., RICH A.;
POTTS J.T. JR., RICH A.;
PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 32-115.
MEDLINE: 71063634.
BREWER H.B. JR., RONAN F.
PROC. NATL. ACAD. SCI. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 82037785.
WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 32-115.

MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAI

AURBACH G.D., POTTS J.T. JR.;

HOPPE-SEYLER'S Z. PHYSIOL. CH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 26-115.

MEDLINE; 74142666.

MEDLINE; 74142666.

MAILTON J.W., NIALL H.D., JACOBS J.W., KEUTMAN COHN D.V.;

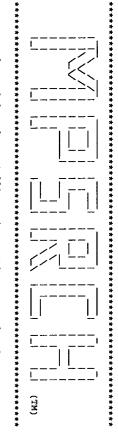
COHN D.V.;

COHN D.V.;

COHN D.V.;

COHN D.V.;
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MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
                                                                                                                                                                      CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                        PROSITE;
HORMONE;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHESIS OF 32-65. MEDLINE; 71091588.
                                                                                                                                                                                                                                        PROPEP
                                          8
                           KLQDVHNFVAL 68
    KLODVHNFVAL 11
                                                                                   h 100.0%;
Similarity 100.0%;
11; Conservative
                                                                                                                                                                                                                                                                                   SIGNAL.
                                                                                                                                                                                                                                                                                                       PS00335; PARATHYROID;
                                                                                                                                                                         26
32
106
115 AA;
                                                                                                                                                                           25
31
115
V
106
V
12980 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.;
U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KISSIL M.S., MEAD D.A., KEMPER B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAUER R., HOGAN M.L., DAWSON B.F.,
                                                                                          Score 79; DB 1; L
Pred. No. 1.01e-06;
0; Mismatches 0
                                                                                                                                                                             PARATHYROID HORMONE
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEUTMANN H.T., POTTS J.T. JR.,
                                                                                                                                           Length 115;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE SALTS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHARP P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAUER R.,
                                                                                                       0
                                                                                                       Gaps
                                                                                                          0
```

search completed: Thu Jul 30 10:45:20 1998
Job time : 7 secs.



(Psrch_pp 900 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:45:37 1998; MasPar time 3.84 Seconds 120.566 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: >US-08-817-547A-21 (1-11) from US08817547A.pep 79

Sequence: 1 KLQDVHNFVAL 11

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 24.328; Variance 30.213; scale 0.805

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

200 200 200 200 200 200 200 200 200 200	Result
55555555555555555555555555555555555555	Score
84.66.65.81 63.33.33.66.66.87 63.33.33.66.66.81	% Query Match
105 207 1325 345 345 345 345 345 345 345 345 345 34	Length
111011111111111111111111111111111111111	ВB
063473 039628 0317622 098474 021349 021349 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 046666 0466666 0466666 0466666 0466666 0466666 04666666 0466666666	ΙΒ
PARATHYROID HORMONE (FORF36L. VINCULIN. SIMILAR TO BACTERIOPHA D8035.17P. K08E7.9. STBA. HYD GAMMA. URA? CTP SYNTHETASE. SIMILAR TO MULTIDRUG-R RNA-DEPENDENT RNA POLY ARYLALKYLAMINE N-ACETY HYDROGENASE SMALL SUBU FERROCHELATASE (EC 4.9 MACROPHAGE METALLOELAS STROMELYSIN-1/2-A. PREPRO-HORMONE CONVERT NEUROENDOCRINE CONVERT PC2. SIMILAR TO THE ATP-BIN	Description
3.43e-03 7.88e-02 2.47e+00 3.95e+00 6.29e+00 9.94e+00 9.94e+00 9.94e+00 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01	Pred. No.

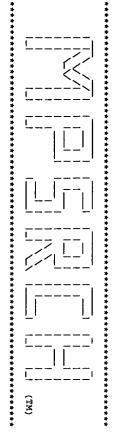
45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21
48	48	48	48	<b>4</b> 8	48	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	50	50	50
•	•	60.8	60.8	60.8	60.8	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	63.3	63.3	63.3
1289	787	693	453	377	232	1918	1774									455	299	227	227					
w	9	12	۲	w	ø	ω	w	4	12	12	w	ω	ω	w	4	10	ω		4	4	w	12	12	ω
001495	032799	Q90719	Q04934	017273	P95776	Q93637	Q93636	Q28689	Q92072	P79922	Q20187	017305	P91676	Q27936	Q28397	P97869	Q19742	Q28973	Q28972	Q28974	Q19123	Q98918	Q08476	Q26599
SIMILARITY TO THE ATP-	PYRUVATE FORMATE-LYASE	OVARIAN FOLLICLE-STIMU	HYPOTHETICAL 50.0 KD P	T27A1.2 PROTEIN.	DNA FOR DTDP-RHAMNOSE	F29G6.3A.	F29G6.3B.	EPITHELIAL BASOLATELAR	MODIFICATION METHYLASE	≫	F39B1.1 (FRAGMENT).	ZK250.1 PROTEIN.	MCM5 HOMOLOG.	ATP-BINDING CASSETTE P	MATRIX METALLOPROTEINA	MICROSOMAL EPOXIDE HYD	SIMILAR TO SER/THR PRO		CYTOCHROME P450 2C33V1	CYTOCHROME P450 2C33V3	SIMILARITY TO CLATHRIN	Ê	CONNECTIN (TITIN) (FRA	SMDR2.
3.78e+01	٠	3.78e+01	3.78e+01	3.78e+01		2.44e+01			2.44e+01	2.44e+01	2.44e+01		2.44e+01	2.44e+01	2.44e+01	2.44e+01	2.44e+01	2.44e+01	2.44e+01	2.44e+01	2.44e+01	1.56e+01	1.56e+01	

RA RA SQ	RN OCC	Db Qy	ST T D R R R R R R C C C C S C C C C C C C C C	DE D
SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  JEHLE J.A., VAN DER LINDEN I.F.A., VLAK J.M.;  VIRUS RES. 0:0-0(1997).  EMBL; AF002732; G2233189;  SEQUENCE 207 AA; 23915 MW; D2F0E988 CRC32;	RESULT 2  PRELIMINARY; PRT; 207 AA.  AC 039628;  OT 01-JAN-1998 (TREMBLREL. 05, CREATED)  DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  DE 0RF36L.  DE 0RF36L.  OS CYDIA POMONELLA GRANULOVIRUS.  OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS.	Query Match  84.8%; Score 67; DB 10; Length 105;  Best Local Similarity 81.8%; Pred. No. 3.43e-03;  Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  48 KLQDGHNFVSL 58	H 28 00 02 E	RESULT 1  10 063473  AC 063473;  AC 063473;  DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  DT 01-VAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

```
Query Match
Query Match
PREST Local Similarity 66.7%; Pred. No. 7.88e-02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 144 RLQEVHDFV 152
:||:||:||
Qy 1 KLQDVHNFV 9

Search completed: Thu Jul 30 10:46:08 1998
Job time: 31 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:50:05 1998; MasPar time 2.64 Seconds
58.155 Million cell updates/sec

#4+10. VIC-08-817-5/71-22

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A.pep
Perfect Score: 72

Sequence: 1 LQDVHNFVAL 10

Scoring table: PAM 150 Gap 15

earched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseg31-2

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.979; Variance 58.346; scale 0.291

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description	Pred. No
р ;	72	100.0	38	ٔ و	R58151	[Ser22]-hPTH(1-38)-OH	8.81e-01
N	72	100.0	38	9	R58153	-hPTH(1-38)	
ω	72	100.0	38	9	R58022	[Ilel]-hPTH(1-38)-OH.	
4	72	100.0	38	9	R58140	1]-hPTH(1-38	
տ	72	100.0	38	9	R58142	[Asn21]-hPTH(1-38)-OH	
σ	72	100.0	38	9	R58129	[His19]-hPTH(1-38)-OH	
7	72	100.0	38	9	R58133	[Asp19]-hPTH(1-38)-OH	8.81e-01
œ	72	100.0	44	26	P30015	Human parathyroid hor	
9	72	100.0	47	25	W21946	Fusion protien compri	8.81e-01
10	72	100.0	84	27	W25687	٥	8.81e-01
11	72	100.0	84	4	R23237	Human parathyroid hor	8.81e-01
12	72	100.0	84	4	R21192	Human parathyroid hor	8.81e-01
13	72	100.0	84	4	R23309	Bovine parathyroid ho	8.81e-0
14	72	100.0	84	4	R23276	Bovine parathyroid ho	8.81e-01
15	72	100.0	84	4	R21254	Human parathyroid hor	8.81e-01
16	72	100.0	84	4	R23429	Porcine parathyroid h	8.81e-0
17	72	100.0	84	4	R23259	Bovine parathyroid ho	8.81e-0
18	72	100.0	84	4	R23485	Porcine parathyroid h	8.81e-01
19	72	100.0	84	4	R21257	Human parathyroid hor	8.81e-01

4	4	4	42	4	4	ω	ىپ	ω	ω	ω	ω	ω	ω	ω	w	Ŋ	2	Ŋ	2	2	Ņ	2	Ŋ	2	
72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	1
100.0	•	•	100.0	٠	•		•		•	•	•	•	•	•	•	•		•	•	•		•	•		٠
115	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	
			4																						
P40251	R23449	N	18	R23363	R23456	R21250	R23248	R23264	R23507	R23227	R21181	R21229	R23242	R23294	R23301	R23272	R23339	R29561	υī.	Ν	8	56	R29568	8	20104
sequence	parathyro:	Porcine parathyroid h	Human parathyroid hor	Bovine parathyroid ho	Porcine parathyroid h	Human parathyroid hor	Human parathyroid hor	Bovine parathyroid ho	Porcine parathyroid h	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	W	Bovine parathyroid ho	Oxidation resistant P	Oxidation resistant [	Human parathyroid hor	id	tant	Oxidation resistant [	d	LOTOTOR Paracity TOTO II
.81e	. 81e	.81e	8.81e-01	.81e	.81e	.81e	.81e	.81e	.81e	. 81e	.81e	.81e	.81e	· C F C											

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밁
                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                           12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-001693.

19-APR-1993; GB-007673.
                                                                                                                                                                                                    (SANO) SANDOZ PATENT GMBH.
(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
Albert R, Bauer W, Breckenridge R, Ca
Gombert F, Gram H, Lewis I, Ramage P,
Waelchli R, Rainer A;
WPI; 94-018352/03
                                                                                                     New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 148; Page 40; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                             where calcium fixation hypoparathyroidism. Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      GB2269176-A.
02-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R58151;
20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R58151 standard; peptide;
                                                                                                                                                                                                                                                                                   (BAUE/)
                                                                                                                                                                                                                                                                                                  SANO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [Ser22]-hPTH(1-38)-OH.
28 lqdvhnfval 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parathyroid hormone; hPTH; variant;
im; depletion; fixation; resorption;
                                                                                                                                                                                                                                                                                                 SANDOZ LTD.
                                                                                                                                                                                                                                                                                   BAUER W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
                       Score 72; DB 9; Lei
Pred. No. 8.81e-01;
0; Mismatches 0;
                                                                                                                                                                                                                                ט'
                                                                                                                                                                                                                                             Cardinaux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analogue;
osteopathy; osteoporosis;
                                                                                                                                                                                                                               dinaux F;
Schneider
                                                  Length
                          Indels
                                                                                                                                                                                                                                Ξ
                          0
                          Gaps
                          0;
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Search completed: Thu Jul 30 10:50:20 1998
Job time : 15 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 02-FEB-194.

PF 12-JUL-1993; 014384.

PF 12-JUL-1993; 014384.

PR 15-JUL-1992; GB-015009.

PR 18-DEC-1992; GB-026415.

28-JAN-1993; GB-026859.

28-JAN-1993; GB-026859.

28-JAN-1993; GB-026691.

28-JAN-1993; GB-001691.

PR 14-APR-1993; GB-001692.

PR 19-APR-1993; GB-001692.

PR (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ PATENT GMBH.

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Gombert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gram H, Lewis I, Ramage P, Schneider H;

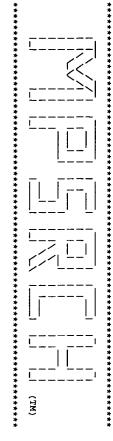
PR Waelchli R, Rainer A;

PR Waelchli R, Rainer A;

PP P Waelchli R, Rainer A;

PP P Waelchli B an example of a highly generic formula covering conditions associated with calcium depletion/resorption, in cases Sequence 38 AA;

Sequence 38 AA;
                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESOLT
ID RS
AC RS
                                                                                                                                                                                              28 lqdvhnfval 37
                                                                                                                                                        1 LODVHNEVAL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R58153; standard; peptide; 38 AA.
R88153;
20-SEP-1994 (first entry)
[Arg26]-hpH(1-38)-OH.
Human parathyroid hormone; hPHH; variant; analogue;
hypoparathyroidism.
Synthetic.
Synthetic.
Calcons: depletion; fixation; resorption; osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LQDVHNFVAL 10
                                                                                                                                                                                                                                                   Score 72; DB 9; Length 38;
Pred. No. 8 81e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           0;
```



Psrch_pp 9 :: protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:49:12 1998; MasPar time 3.29 Seconds 111.059 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-22 (1-10) from US08817547A.pep 72 1 LQDVHNFVAL 10

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

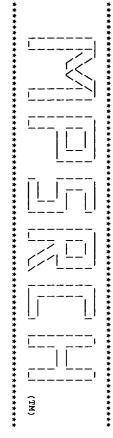
Statistics: Mean 23.774; Variance 33.625; scale 0.707

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query	Length	BG BG	Ħ	Description	Pred. No.
ш.	72	100.0	34	5	1ZWE	parathyroid hormone (	1.05e-03
2	72	100.0	34	5	1 ZWG		1.05e-03
ω	72	100.0	34	U	12WF	parathyroid hormone 4	1.05e-03
4	72	100.0	35	ъ	1ZWD	parathyroid hormone (	1.05e-03
տ	72	100.0	36	Ç,	1ZWB	parathyroid hormone (	1.05e-03
თ	72	100.0	37	σ	1HPH	parathyroid hormone f	1.05e-03
7	72	100.0	37	5	1ZWC	parathyroid hormone (	1.05e-03
<b>&amp;</b>	72	100.0	115	μ.	PTHU	parathyroid hormone p	1.05e-03
9	72	100.0	115	N	JC4202	parathyroid hormone -	1.05e-03
10	72	100.0	115	μ	PTPG	parathyroid hormone p	1.05e-03
11	72	100.0	115	μ	PTBO	parathyroid hormone p	1.05e-03
12	70	97.2	115	N	A05091	parathyroid hormone p	2.81e-03
13	60	•	105	2	151851	<pre>parathyroid hormone -</pre>	3.11e-01
14	53	73.6	34	σ	12WA	parathyroid hormone (	6.64e+00
15	53	73.6	34	u	1HTH	cyclic parathyroid ho	6.64e+00
16	53	73.6	632	N	S73824	3	6.64e+00
17	52	•	606	N	S13526	hydrogenase homolog,	1.01e+01
18	51	70.8	201	N	C65188	hypothetical 22.3 kD	1.53e+01
19	50	69.4	217	N	E70126		2.29e+01
20	50	69.4	543	N	H40781	hypothetical 60.7K pr	2.29e+01
21	50	69.4	543	N	S25128		2.29e+01
22	50	69.4	653	N	S40449	8	
23	50	69.4	731	N	S28491	hypothetical protein	2.29e+01

45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	4.4
47	47	48	48	48	48	48	48	48	48	48	48	48	48	49	49	49	49	49	49	49	Ċ
65.3	65.3	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7			68.1				68.1	
494	240	1612	1318	881	653	471	471	452	398	328	326	145	136	1537	1495	1490	1321	455	316	142	100
N	N	N	-	Н	N	N	ω	N	N	N	N	ۍ	N	N	N	N	N	N	N	N	
S13101	F64676	JC5210	HIBPD7	WZBE55	S27270	A46400	A43480	S77436	D69953	A43598	S76954	1ATO	S73520	JC4172	S22610	JC5145	S27337	A26081	S07569	B40535	030034
cytochrome P450 c117	biotin synthesis prot	DNA (cytosine-5-)-met	internal virion prote	gene 55 protein - hum	prohormone convertase	segment polarity prot	segmentation gene hed	sigma factor sibG reg	conserved hypothetica	L-lactate dehydrogena	hypothetical protein	17-hedgehog 17-kda fr	MG441 homolog E09_orf	DNA (cytosine-5-)-met	DNA (cytosine-5-)-met	DNA (cytosine-5-)-met	multidrug resistance	epoxide hydrolase (EC	protein H5 - slime mo	hrin-associ	ATPC 2 TESTON INTERNAL
7.52e+01	7.52e+01	5.09e+01	5.09e+01	5.09e+01	5.09e+01	3.43e+01	3.43e+01	3.43e+01	3.43e+01	3.43e+01	3.43e+01	3.43e+01	4.43C+01								



(Psrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:47:53 1998; MasPar time 2.15 Seconds 116.508 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-22 (1-10) from US08817547A.pep

1 LQDVHNFVAL 10

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 24.901; Variance 27.707; scale 0.899

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description Pred.  PIHY_CANFA PARATHYROID HORMONE PR 2.56 PIHY_BOVIN PARATHYROID HORMONE PR 2.56 PIHY_PIG PARATHYROID HORMONE PR 2.56 PIHY_PIG PARATHYROID HORMONE PR 2.56 PIHY_LAT PARATHYROID HORMONE PR 2.56 PIHY_RAT PARATHYROID HORMONE PR 2.56 PIHY_RAT PARATHYROID HORMONE PR 3.51 Y242_MYCPN HYPOTHETICAL PROTEIN M 1.14 Y262_MYCPN HYPOTHETICAL PROTEIN M 5.08 APIJ_HUWAN CLATHRIN COAT ASSEMBLY 8.24 APIJ_RAT VEGETATIVE SPECIFIC PR 8.24 MYEDE_RAT WEGETATIVE SPECIFIC PR 8.24 MYEDE_RAT MULTIDRUG RESISTANCE P 8.24 MYEDE_RAT MULTIDRUG RESISTANCE P 8.24 Y441_MYCPN HYPOTHETICAL PROTEIN M 1.32
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
<b>4</b> 5	45	45	45	45	<b>4</b> 5	45	45	<b>4</b> 5	45	46	46	46	46	47	47	47	47	47	47	47	47
62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	63.9	63.9	63.9	63.9					65.3			
2505	2504	1247	687	505	490	303	297	120	104	4344	964	469	435	1444	925	700	589	494	274	251	125
۳	<u> </u>	μ	_	Н	ш	<u> </u>	بر	Н	μ-	ب	۲	-ر	۲	۲	Ь	μ,	4	۳	سر	Н	Н
FAS_RAT	FAS_HUMAN	YMF6_CAEEL	CSTA_HELPY	YXD2_CAEEL	CPCQ_MESAU	APPC_BACSU	YMY9_YEAST	YGX0_YEAST	YHV2_LACHE	DYHC_EMENI	YBS9_YEAST	NIFN_RHISN	PEPC_LACIC	RRPL_RDV	DBL_HUMAN	ADB1_YEAST	KY28_MYCTU	CPCN_RAT	CD1_SYLFL	AGAI_ECOLI	Y4WJ_RHISN
SYNTHASE	FATTY ACID SYNTHASE (E	HYPOTHETICAL 139.9 KD	CARBON STARVATION PROT	PUTATIVE SERINE CARBOX	CYTOCHROME P450 IIC26	OLIGOPEPTIDE TRANSPORT	HYPOTHETICAL 34.0 KD P	HYPOTHETICAL 14.1 KD P	HYPOTHETICAL 11.8 KD P	DYNEIN HEAVY CHAIN, CY	HYPOTHETICAL 110.3 KD	NITROGENASE IRON-MOLYB	AMINOPEPTIDASE C (EC 3	RNA-DIRECTED RNA POLYM	PROTO-ONCOGENE DBL PRE	PROBABLE BETA-ADAPTIN	PROBABLE SERINE/THREON	CYTOCHROME P450 IIC23	T-CELL SURFACE GLYCOPR	PUTATIVE GALACTOSAMINE	HYPOTHETICAL 13.3 KD P
5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	3.34e+01	3.34e+01	3.34e+01	3.34e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01

288	ää	걸	ĮĮ.	g	AC	H	: R	Qy	đđ			SC	FT	ΉŢ	Ξ	Ş.	DR	ᄗ	S	S	RL	묫	RA	RX	25	RP	RN	8	გ	တ္တ	GN	멅	ij	걸	ဌ	Ã	ij	RE
S EJEA: S BOS TAURUS (BOVINE). C EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		01-NOV-1997 (REL.	21-JUL-1986 (REL. 01,	21-JUL-1986 (REL.	P01268;		SULT 2	בי	b 59 LQDVHNFVAL 68	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; Score 72; DB 1; Length 115; ; Pred. No. 2.56e-05;	SEQUENCE 115 AA;	CHAIN 32 115 PAF	PROPEP 26 31 BY	SIGNAL 1 25	HORMONE;		EMBL; U15662; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION.	-:-	GENE 160:241-:	DEWILLE J.W., CAPEN C.C						EUTHERIA; CARNIVORA.	EUKARYOTA; METAZO	S CANIS FAMILIARIS (DOG).	PTH.	PARATHYROID HORMONE PF	01-OCT-1996 (REL. 34, LAST ANNOTATION	01-OCT-1996 (REL. 34,	01-OCT-1996 (REL.	P52212;	PTHY	RESULT 1

EUTHERIA; ARTIODACTYLA. [1]

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                                    B
                                                                                 RESUMEDLINE; 71091588.

RA SYNTHESIS OF 32-65.

RA POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., PROTTS S.T. JANSON B.F., HOGAN M.L., AURBACH G.D.;

RA DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

RA DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN EMBL; JO0024; B.S., EMBL; JO0024; G.163641; -

EMBL; JO0024; G.163643; -

EMBL; JO0024; E.18259; ALT_SEQ.

DR EMBL; JO0024; E.18259; ALT_SEQ.

DR EMBL; JO0024; E.18259; ALT_INIT.

DR EMBL; JO0038; G.163645; -.

DR PORSITE; PS00335; PARATHYROID; 1.

FT SIGNAL 1

25

FT PROPED 26

SO SEQUENCE 115 AA; 12980 MW; 673EASF2 CRC32;
                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 LQDVHNFVAL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 32-115.

MEDLINE; 71063634.

BREWER H.B. JR., RONAN R.;

PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
         μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 32-115.

MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS(
AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-115.

MEDLINE; 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
COHN D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE; 84262483.

WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER
GENE 28:319-329(1984).

[5]
LQDVHNFVAL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 82037785.
WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

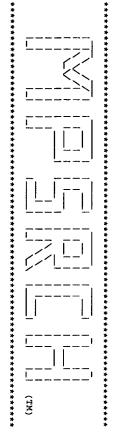
MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                         Score 72; DB 1; Ler
Pred. No. 2.56e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAUER R., HOGAN M.L., DAWSON B.F.,
                                                                  _Length 115;
                                         Indels
                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₩.
                                 Gaps
                                 0
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Search completed: Thu Jul 30 10:47:59 1998 Job time : 6 secs.



Psrch_pp on: protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:48:18 1998; MasPar time 3.79 Seconds 111.185 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: >US-08-817-547A-22 (1-10) from US08817547A.pep

Sequence: 1 LQDVHNFVAL 10

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 23.635; Variance 29.603; scale 0.798

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	!
20 20 20 20 20 20 20	Result
0 D D D D D D D D D D D D D D D D D D D	Score
83.3 79.2 72.2 72.2 72.2 69.4 68.1 68.1 68.1 68.1 68.1 68.1 68.1 68.1	% Query Match
105 207 993 345 666 653 665 142 227 227 227 227 227 227 227 227 227 2	% Query Match Length
110 110 111 110 110 110 110 110 110	DB
Q63473 Q39628 Q39628 Q39628 Q465793 Q46606 Q106972 Q106973 Q19123 Q19123 Q19123 Q19123 Q19123 Q19123 Q19123 Q19123 Q19123 Q19123 Q191349 Q28973 Q191349 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q20187 Q201	ID
PARAPHYROID HORMONE (FORE36L VINCULIN. STBA. HYD GAMMA. HYD GAM	Description
8.41e-02 3.80e-01 1.24e+00 4.22e+00 4.22e+00 4.22e+01 1.06e+01 1.06e+01 1.06e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01	Pred. No.

4 4 5 4	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21
4 6 6	46	46	47	47	47	47	47	47	47	47	47	48	48	48	48	48	48	48	48	48	48	48	48
63.9 63.9	63.9	63.9	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
1758 1825	709	402	1444	950	939	939	620	494	485	240	207	1612	1149	787	787	708	653	542	516	452	440	377	326
10	w	12	11	ω	w	ω	10	10	μ	9	4	w	ω	ø	ø	N	ω	11	ω	9	9	ω	9
Q22830 P97394	015783	042479	Q98631	015788	015790	015799	035488	064534	Q05160	025846	002785	Q27746	Q23315	032799	032797	Q92542	Q25409	011448	Q18198	P73256	Q55301	017273	P74746
SIMILAR TO HUMAN SREBP ACTIN-CROSSLINKING PRO	HYBRID HISTIDINE KINAS	FERROCHELATASE (EC 4.9	×		STRAIN 7G8 CG9 (CG9) A	STRAIN DD2 HEAT SHOCK		CYTOCHROME P450 (EC 1.	ALPHA-AGGLUTININ (AG-A	BIOTIN SYNTHESIS PROTE	ARYLALKYLAMINE-N-ACETY	MODIFICATION METHYLASE	ZC434.5.	PYRUVATE FORMATE-LYASE	PYRUVATE FORMATE-LYASE	MYELOBLAST KIAA0253 (F	STAGNALIS LPC2.	VP78.	SIMILAR TO K12H4.7 AND	SIGMA FACTOR SIBG REGU	COTA GENE (ORF440), CO	T27A1.2 PROTEIN.	HYPOTHETICAL 36.0 KD P
6.22e+01 6.22e+01	6.22e+01	6.22e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01		2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	•	2.61e+01		2.61e+01	2.61e+01	2.61e+01

	RESULT 2  ID 039628 AC 039628; DT 01-JAN-1998 (TREMBLREL 05, DT 01-JAN-1998 (TREMBLREL 05, DT 01-JAN-1998 (TREMBLREL 05, DT 01-JAN-1998 (TREMBLREL 05, DE 0RF36L.	Matches 8; Conservative  Db 49 LQDGHNFVSL 58            Qy 1 LQDVHNFVAL 10	atch cal Similarity	[1] SEQUENCE FROM N.A. TISSUE-THYROID, AN TISSUE-THYROID, AN SCHMELLER H.J., GRR ADV. GENE TECHNOL. EMBL; M54875; G601 NON_TER 1 SEQUENCE 106 AA.	OC EUTHERIA; RODENTIA.	Q63473; 01-NOV-1996 01-NOV-1996 01-JAN-1998 PARATHYROID	
ES, NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS. LINDEN I.F.A., VLAK J.M.; 7). 2189; 23915 MW; D2F0E988 CRC32;	PRELIMINARY; PRT; 207 AA. EMBLREL. 05, CREATED) EMBLREL. 05, LAST SEQUENCE UPDATE) EMBLREL. 05, LAST ANNOTATION UPDATE) GRANULOVIRUS.		mw; bAC3163E CKC32; ; Score 60; DB 10; Length 105; ; Pred. No. 8.41e-02;	.RATHYROID; G., MAYER H.; 228-229(1984). 	(RAT). ; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 	01, CREATED) 01, LAST SEQUENCE 05, LAST ANNOTAT AGMENT).	PRELIMINARY; PRT; 105 AA.

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Query Match

Best Local Similarity 75.0%; Pred. No. 3.80e-01;

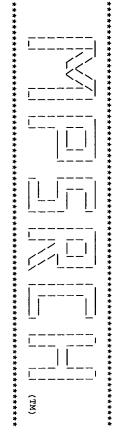
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 145 LOPYHDFV 152

Qy 1 LOPYHDFV 8

Search completed: Thu Jul 30 10:48:55 1998

Job time: 37 secs.
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MPsrch_pp in on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:52:34 1998; MasPar time 2.61 Seconds 52.799 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-23 (1-9) from US08817547A.pep 64 1 QDVHNFVAL 9

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part5 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.221; Variance 50.458; scale 0.321

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
00000000000000000000000000000000000000	Score
11111111111111111111111111111111111111	Query Match L
6 C C C C C C C C C C C C C C C C C C C	Length DB
R58151 R58142 R58142 R58129 R58129 R58133 P30013 P301132 W22946 W25687 R21192 R23309 R23176 R21154 R21154 R23429 R23429 R23429 R23429	Ħ
[Ser22]-hPTH(1-38)-OH [ASD2]-hPTH(1-38)-OH [Ph22]-hPTH(1-38)-OH [H1519]-hPTH(1-38)-OH [H1519]-hPTH(1-38)-OH [Human parathyroid hor Fusion protien compri- Human parathyroid hor Human parathyroid hor Human parathyroid hor Human parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Dorcine parathyroid hor Porcine parathyroid hor	Description
1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00	Pred. No.

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29

qdvhnfval 37

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	e of a ful	sequence	parathyroid	parathyroid ho	parathyroid	Bovine parathyroid ho	Porcine parathyroid h	Porcine parathyroid h	arathyroid	parathyroid	Human parathyroid hor	Human parathyroid hor	parathyroid	parathyroid	parathyroid	parathyroid	parathyroic	parathyroid	parathyroid	resistant	tion resis	n parathyroid ho	parathyroid ho	resistant	resistant	Ċ

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RESULT
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Search completed: Thu Jul 30 10:52:49 1998 Job time: 15 secs.
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PF 12-JUL-1993; GB-015009.

PR 15-JUL-1992; GB-026415.

PR 18-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-001691.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001691.

PR 14-APR-1993; GB-001692.

PR 14-APR-1993; GB-001692.

PR 14-APR-1993; GB-001693.

PR (SANO) SANDOZ LTD.

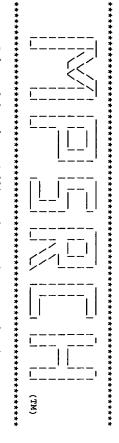
PA (SANO) SANDOZ PATENT CMBH.

PA (SANO) SANDOZ CMBH.

PA (SANO) SANDOZ CMBH.

PA (SANO) SANDOZ CMBH.

PA (SANO) 
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Best Local Similarity 100.0%;
Matches 9; Conservative
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[Asn21]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R58142 standard; peptide; 38 R58142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypoparathyroidism.
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                                                                                                                                                                                                  QDVHNFVAL 9
                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 9; Ler
Pred. No. 1.84e+00;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                      0,
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:51:51 1998; MasPar time 3.32 Seconds
99.175 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-23 (1-9) from US08817547A.pep 64 1 QDVHNFVAL 9

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 22.614; Variance 30.162; scale 0.750

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

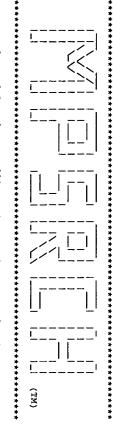
# SUMMARIES

	: 1
222 232 232 243 254 255 257 257 257 257 257 257 257 257 257	No.
00000000000004444444444444444444444444	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	- G7
34 34 35 36 37 37 37 37 37 37 37 37 37 37 37 37 37	Length
NNNUUUNNNNNNNHHNHUUUUU	BB
1ZWE 1ZWE 1ZWB 1ZWD 1ZWD 1ZWB 1HPH 1HPH 1HPH 1ZC4202 PTPO PTPO A05091 151851 C651851 C651868 A260818 A260818 B373520 B45883 A26083 B37145 A64700 A38233	ID
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67.2	67.2	67.2	67.2	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	70.3	70.3	70.3	70.3	70.3	70.3	70.3	۷. ن
1550	1071	522	219	670	669	654	606	387	326	315	227	211	140	2509	2505	2504	2504	917	687	632	167
N	N	N	N	Н	_	N	N	N	N	N	N	N	N	N	ب	N	2	N	N	Ν	^
S60228	S44798	S77073	B64153	SYASAA	JN0781	S54289	S13526	JC2032	S76954	S33143	S33956	H64961	A69445	G01880	XYRTFA	B57788	A57788	S40178	H64665	S73824	500080
glutamate synthase (f	F09G8.5 protein - Cae	hypothetical protein	ribose-5-phosphate is	acetateCoA ligase (	acetateCoA ligase (	phosphoglycerate kina	hydrogenase homolog,	regulatory protein Ac	hypothetical protein	superantigen Mtv - mo	-		hypothetical protein	fatty-acid synthase (	<pre>fatty-acid synthase (</pre>	fatty-acid synthase (	fatty-acid synthase (	isoleucinetRNA liga	carbon starvation pro	MG242 homolog H91_orf	nypornerical procein
1.43e+02	1.43e+02	1.43e+02	1.43e+02	9.57e+01	9.57e+01	9.57e+01	9.57e+01		•		9.57e+01		9.57e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	b. Jbetul

REFERENCE #authors #book COMMENT I	ORGANISM REFERENCE #authors #submission #cross_refe	co co	RESULT 2 ENTRY TITLE	Db 26 QI   1   1   1   1   1   1   1   1   1   1	Query Match Best Local : Matches	FEATURE 15-25 SUMMARY	w	#authors #book	REFERENCE #submission #cross-refe #cross-refe	ORGANISM	TITLE ALTERNATE_NAMES	RESULT 1
TN003319  Marx, U.C.  Marx, U.C.  In Strukturen Verschiedener Parathormonfragmente in Loesung,  pp.0, Bayreuth: University of Bayreuth (Thesis), 1996  Resolution: not applicable	1	synthetic _NAMES n-succinyl-hpth(4-37) _succinyl human parathyroid hormone 4-37, NMR, 10 structures	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	QDVHNEVAL 34           QDVHNEVAL 9	y Match 100.0%; Score 64; DB 5; Length 34; Local Similarity 100.0%; Pred. No. 9.27e-03; hes 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR hormone	C. turen Verschiedener Parathormonfr <b>a</b> gmente in	#AUTHORS ROSSCH, P.; MARX, U.C. #AUTHORS ROSSCH, P.; MARX, U.C. #Submission submitted to the Brookhaven Protein Data Bank, June 1996 #SCROSS-references DDB:1ZWE TNO1721	l_name Homo sapiens #common_name man	parathyroid hormone (residues 4-37) - h HPTH(4-37)	

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MPsrch_pp 02: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:50:38 1998; MasPar time 2:13 Seconds 106.097 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-23 (1-9) from US08817547A.pep 64 1 QDVHNFVAL 9

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.654; Variance 24.782; scale 0.954

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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A POTTS J.T. JREGEAR G.W., AUTHAUM H.T., NIALL H.D., SAUER R.,

A POTTS J.T. JREGEAR G.W., AUTHAUM H.T., AUTHAUM H.T., NIALL H.D., SAUER R.,

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HORMONE;
SIGNAL
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MEDLINE; 71063634.

BREWER H.B. JR., RONAN R.;

BREWER H.B. JR., RONAN R.;

BREWER H.B. JR., RONAN R.;

BREWER H.B. JR., RONAN R.;
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MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSO AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
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MEDLINE; 74142666.

HAMMLITON J.W., NIALL H.D., JACOBS J.W., KEUTMANN COHN D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
POTTS J.T. JR., RICH A.;
PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
60 QDVHNFVAL 68
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1 QDVHNFVAL 9
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MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
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MEDLINE; 82037785.
MEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
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core 52; red. No. 1; Misma	PRT ST ST VER 198	3400 4746 44746 44746 44723 3496 33996 33996 33996 4606 6606 6606 6606 6606 6606 6606 6
DB 10; 1.20e+00; tches 1	; 105 AA.  ED) SEQUENCE UPDATE) ANNOTATION UPDATE) TEBRATA; TETRAPODA;  (C3163E CRC32;	RETROVIRIDAE PR HYPOTHETICAL 36 SIMILAR TO BACT SIMILAR TO S. C. HYPOTHETICAL 49 AMYLASE PRECURS ZK849.4. HYD GAMMA. K0827.5. HYD GAMMA K0827.5. HYDOTHETICAL 38 TOGD8 P450 CYTOCHROME P450 CYT
Length 105; ; Indels	) TE) ODA; MAMMALIA;	OTEI
0; 0	LIA;	E, B 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Gaps		. 6.64 6.64 6.64 6.64 6.64 6.64 6.64 6.6
0,		000000000000000000000000000000000000000

RESULT 2

PS5793

AC P95793;

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE STBA.
GN STBA.
GN STBA.
OS SERRATIA MARCESCENS.
OG PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
RN [1]
RP SEQUENCE FROM N.A.
RA WHELAN K.F., BEKKERING M., TAYLOR D.E.;

```
RI SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

DR EMBL; U59131; G1695865; -.

WW PLASMID.

SEQUENCE 345 AA; 38433 MM; E194251E CRC32;

SEQUENCE 345 AA; 38433 MM; E194251E CRC32;

QUETY MAICH

Best Local Similarity 77.8%; Pred. No. 1.20e+00;

Barches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

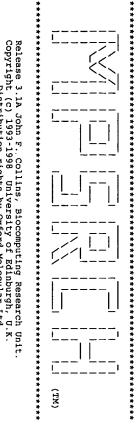
MAICHES 114

Db 116 OPWIFFVIL 124

Qy 1 ODVHNFVAL 9

Search completed: Thu Jul 30 10:51:32 1998

JOB time: 29 secs.
```



Psrch_pp 9 :: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:55:02 1998; MasPar time 2.60 Seconds 47.193 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-24 (1-8) from US08817547A.pep 57 1 DVHNFVAL 8

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.692; Variance 45.953; scale 0.341

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No
1	57	100.0	38	ِ و	R58151	[Ser22]-hPTH(1-38)-OH	5.52e+00
N	57	100.0	38	9	R58142	[Asn21]-hPTH(1-38)-OH	5.52e+00
ω	57	100.0	38	φ	R58140	[Phe21]-hPTH(1-38)-OH	5.52e+00
4	57	100.0	38	٥	R58129	[His19]-hPTH(1-38)-OH	5.52e+00
ហ	57	100.0	38	9	R58133	[Asp19]-hPTH(1-38)-OH	5.52e+00
0	57	100.0	44	26	P30015	Human parathyroid hor	5.52e+00
7	57	100.0	47	25	W21946	Fusion protien compri	5.52e+00
8	57	100.0	84	27	W25687	Human parathyroid hor	5.52e+00
9	57	100.0	84	4	R23227	Human parathyroid hor	5.52e+00
10	57	100.0	84	4	R21181	Human parathyroid hor	5.52e+00
11	57	100.0	84	4	R23276	Bovine parathyroid ho	5.52e+00
12	57	100.0	84	4	R21254	Human parathyroid hor	5.52e+00
13	57	100.0	84	4	R23429	Porcine parathyroid h	5.52e+00
14	57	100.0	84	4	R23259	Bovine parathyroid ho	5.52e+00
15	57	100.0	84	4	R23444	Porcine parathyroid h	5.52e+00
16	57	100.0	84	4	R23281	Bovine parathyroid ho	5.52e+00
17	57	100.0	84	4	R23424	Porcine parathyroid h	5.52e+00
18	57	100.0	84	4	R23383	Porcine parathyroid h	5.52e+00
19	57	100.0	84	4	R21161	Human parathyroid hor	5.52e+00

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30 dvhnfval 37

Query Match 100.0%; Best Local Similarity 100.0%; Matches 8; Conservative

Score 57; DB 9; Length 38; Pred. No. 5.52e+00; 0; M1smatches 0; Indels

0;

Gaps

0;

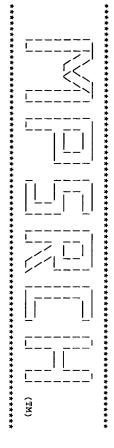
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DVHNFVAL

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RESULT
ID REAL
AC REAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 02-FEB-1994.
PP 12-JUL-1993; 014384.
PF 12-JUL-1993; GB-015009.
PR 15-JUL-1992; GB-025859.
PR 23-DEC-1992; GB-026859.
23-DEC-1992; GB-026859.
28-JAN-1993; GB-001691.
28-JAN-1993; GB-001691.
28-JAN-1993; GB-001692.
PK 14-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ GRATINT GMBH.
PA (SANO) SANDOZ GRATINT GMBH.
PA (SANO) SANDOZ GRATINT GMBH.
PA (SAN
                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 2
R58142 standard; peptide; 38 AA.
R58142;
R58142;
20-SEP-1994 (first entry)
[Asn21]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypoparathyroidism.
30 dvhnfval 37
|||||||
1 DVHNFVAL 8
                                                                                                                                                                                                                          Score 57; DB 9; Ler Pred. No. 5.52e+00; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                     Length 38;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           0;
```

Search completed: Thu Jul 30 10:55:16 1998 Job time : 14 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:54:14 1998; MasPar time 3.34 Seconds 87.598 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-24 (1-8) from US08817547A.pep 57 1 DVHNFVAL 8

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.941; Variance 28.147; scale 0.780

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 3 3 3 3 3 4 4 4 4 4 7 7 6 5 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	No.
4 4 4 4 4 4 4 4 4 5 7 7 7 7 7 7 7 7 7 7	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query
34 34 34 35 36 37 37 37 115 115 115 115 115 115 115 274 1520 105 207 207 207 207 207 207 207 207 207 207	Length
H N N N N N N N N N N N H H N H M M M M	BB
12WE 12WG 12WG 12WG 11ZWD 11ZWD 11ZWC 11ZWC 11ZWC 11ZWC 104202 104202 104202 105200 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 1053030 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 10530 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 10530 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105300 105	뷰
parathyroid hormone ( parathyroid hormone 4 parathyroid hormone ( parathyroid hormone (1) hypothetical 12% hlv-parathyroid hormone (1) parathyroid hormone (1) hypothetical protein carbon starvation profatty-acid synthase ( fatty-acid synthase ( fatty-acid synthase (	Description
1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.14e-01 1.1	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
42	42	42	42	42	42	42	42	42	42	42	43	43	43	43	43	43	43	44	44	44	4
73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	75.4	75.4	75.4	75.4	75.4	75.4	75.4	77.2	77.2	77.2	78.9
1321	316	212	212	208	207	182	182	182	182	178	2512	962	760	444	309	302	219	632	227	140	6007
N	ພ	N	N	بر	N	σ	ហ	ഗ	u	σı	Ц	N	N	N	2	ν	N	N	N	N	
S27337	S07569	A54204	A40047	CSHUB	A40516	2RMCA	2RMCG	2RMCC	2RMCE	1CYNA	XYCHFA	S67385	151720	A41842	B38545	A55723	B64153	S73824	S33956	A69445	COTABO
multidrug resistance	protein H5 - slime mo	peptidylprolyl isomer	peptidylprolyl isomer	peptidylprolyl isomer	peptidylprolyl isomer	Cyclophilin c complex	a	ი	Cyclophilin c complex	cyclophilin b, chain	fatty-acid synthase (	hypothetical protein	probable DNA helicase	lysine/cadaverine ant	hypothetical protein	dodecenoyl-CoA Delta-	ribose-5-phosphate is	MG242 homolog H91_orf	ubiquitin thiolestera	hypothetical protein	ratty-acid synthase (
1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01			5.24e+01	5.24e+01	5.24e+01	S.Sye+UI

RESULT 2  ENTRY  PARATHYPOID HOTMONE 4 37 MUTANT N-TERMINAL SUCCINYL Synthetic  ALTERNATE_NAMES n-succinyl-hpth(4-37)  ORGANISM #formal_name synthetic  REFERENCE A67743  # submission submitted to the Brookhaven Protein Data Bank, June #cross-references PDB:LIMG  REFERENCE TN003319  # authors submission fragmente in Strukturen Verschiedener Parathormonfragmente in Strukturen Verschiedener Parathormonfragmente in pp.0, Bayreuth: University of Bayreuth (Thesis),  COMMENT Resolution: not applicable	Db 27 DVHNFVAL 34           Qy 1 DVHNFVAL 8	Query Match 100.0%; Score 57; DB 5; Leng Best Local Similarity 100.0%; Pred. No. 1.14e-01; Matches 8; Conservative 0; Mismatches 0;	5 #region helix (right hand alphe #length 34 #molecular-weight 4128	rs Resolu Determ	REFERENCE A67860  #authors Roesch, P.; Marx, U.C.  #submission submitted to the Brookhaven Protein Da  #cross-references PDB:1ZWE  REFERENCE TN001721	1 1ZWE #type complete parathyroid hormone (residues 4-37) - NAMES HPTH(4-37) structure of human parathyroid hormon structures , #formal_name Homo sapiens #common_name
lete 37 mutant N-TERMINAL SUCCINYLATED - yroid hormone 4-37, NMR, 10 structures c khaven Protein Data Bank, June 1996 khaven Parathormonfragmente in Loesung, iversity of Bayreuth (Thesis), 1996		01	and alpha) ht 4128 #checksum 5508	Parathormonfragmente in Loesung, ty of Bayreuth (Thesis), 1996	Protein Data Bank, June 1996	es 4-37) - human bid hormone fragment 4-37, NMR 10 common_name man

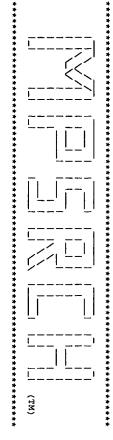
```
COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE #region helix (right hand alpha)\
2-9 #region helix (right hand alpha)\
15-25 #region helix (right hand alpha)\
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 57; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.14e-01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 DVHNFVAL 34
||||||||
Qy 1 DVHNFVAL 34
|||||||
Qy 1 DVHNFVAL 8

Search completed: Thu Jul 30 10:54:45 1998

Search completed: Thu Jul 30 10:54:45 1998
```



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:53:07 1998; MasPar time 2.11 Seconds 94.946 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-24 (1-8) from US08817547A.pep 57 1 DVHNFVAL 8

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.974; Variance 23.185; scale 0.991

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 110 110 110 1110 1110 1110 1110 11	sult No.
	Score
100 0 100 0 100 0 0 100 0 0 0 0 0 0 0 0	% Query Match
115 115 115 115 115 116 274 104 274 275 287 2504 2504 2504 2504 2505 2504 2505 2504 2505 2506 275 277 277 277 277 277 277 277 277 277	Length
444444444444444444444444444444444444444	BB
PTHY_CANFA PTHY_BOVIN PTHY_FIG PTHY_HUMAN PTHY_RAT Y441_MYCPN Y1GP_ECOLI CD1_SYLF1 YHV2_LACHE YHV2_LACHE YHV2_LACHE YHV2_LACHE YHV3_HALP YHAS_HUMAN FAS_RAT ML11_BRARE UBL_DROME Y4XG_MCIN RPIA_HEIPN Y4XZ_MCHN RPIA_HEIPN RPIA_HEIN D3D2_HUMAN RPIA_HEIN D3D2_HUMAN UBG2_COLI CUL1_HUMAN VAXA_SCHPO	Ĥ
PARATHYROID HORMONE PR PARATHYROID HORMONE PR PROTHETICAL 22.3 KD P T-CELL SURFACE GLYCOPR HYPOTHETICAL 34.0 KD P CARBON STARVATION PROT PATTY ACID SYNTHASE (E PATTY ACID SYNTHASE (E PATTY ACID SYNTHASE (E MELATONIN RECEPTOR TYP UBIQUITIN CARBOXYL-TER HYPOTHETICAL 55.5 KD P HYPOTHETICAL 55.5 KD P HYPOTHETICAL FROTEIN M RIBOSE 5-PHOSPHATE ISO 3,2-TRANS-ENOYL-COA IS PROBABLE KONSTRUCTURAL PROBABLE CADAVERINE/LY CULLIN HOMOLOG 1 (CUL-	Description
8.14e-03 8.14e-03 8.14e-03 8.14e-03 8.14e-03 2.77e-02 2.80e+00 4.80e+00 4.80e+00 8.16e+00 8.16e+00 8.16e+00 8.16e+01 1.37e+01 1.37e+01 1.37e+01 2.29e+01 2.29e+01 2.29e+01 2.29e+01 2.29e+01 2.29e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	43
73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	75.4
1550	1321	1038	1004	830	790	689	541	455	316	294	284	284	212	212	208	208	208	208	207	161	2511
<b>ب</b>	μ	μ	<b>ب</b>	μ.	۲	Н	_	Н	_	Н	$\vdash$	ᆫ	Н	Н	۳	<b>,</b>	ᆫ	Н	Н	<u> </u>	بر
GLTB_SYNY3	MDR1_CAEEL	ATNA_DROME	GCSP_CHICK	MKT1_YEAST	TNP3_HUMAN	YBP3_YEAST	YELL_DROME	HYEP_RAT	VSH5_DICDI	YHBM_ECOLI	YHBJ_ECOLI	YHBJ_KLEPN	CYPC_HUMAN	CYPC_MOUSE	CYPB_MOUSE	CYPB_HUMAN	CYPB_BOVIN	CYPB_RAT	CYPB_CHICK	YCX5_EUGGR	FAS_CHICK
FERREDOXIN-DEPENDENT G	MULTIDRUG RESISTANCE P	SODIUM/POTASSIUM-TRANS	GLYCINE DEHYDROGENASE	MKT1 PROTEIN.	TUMOR NECROSIS FACTOR,	HYPOTHETICAL 77.3 KD P	YELLOW PROTEIN.	EPOXIDE HYDROLASE (EC	VEGETATIVE SPECIFIC PR	HYPOTHETICAL 33.6 KD P	HYPOTHETICAL 32.5 KD P	HYPOTHETICAL 32.5 KD P	PEPTIDYL-PROLYL CIS-TR	HYPOTHETICAL 18.6 KD P	FATTY ACID SYNTHASE (E						
3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	2.29e+01

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PIH. BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	THYROID HORMOI	(REL. 35, LAST	01,	(REL.		PTHY_BOVIN STANDARD; PRT; 115 AA.		1 DVHNEVAL 8	61 DVHNEVAL 68	8; Conservative 0; Misma	Query Match 100.0%; Score 57; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 8.14e-03;	, ,	32 115 PAI	31	1 25 BY			; G558916;	PREVENTING THEIR RENAL EXCRETION.		GENE 160:241-243(1995).	CAPEN C.C.;	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE; 95369696.	TISSUE-PARATHYROID;	SEQUENCE FROM N.A.	[1]			CANIS FAMILIARIS (DOG).		HORMONE PRECUR	(REL. 34, LAST ANNOTATIO	34,	(REL.	12;	PTHY_CANFA STANDARD; PRT; 115 AA.	RESULT 1

EUTHERIA; ARTIODACTYLA.
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SQ SQ
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MEDLINE; 71091588.

A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU APPROCES L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C --- FUNCTION, PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SCI. U.S.A. 68:63-67(1971).

C EMBL; VO0106; G85; --

EMBL; J00024; G163641; --

EMBL; J00024; G163643; --

EMBL; J00024; G163647; --

REMBL; J00024; G163647; --

REMBL; K01938; G163647; --

REMBL; M25082; G163647; --

REMBL; M25082; G163645; --

REMBL; M25082; G163645; --

REMBL; M25082; G163645; --

REMBL; M25082; G163645; --
                                                Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE: 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NAT POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 82037785.
WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-115.

MEDLINE; 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN COHN D.V.;

CON D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
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MEDLINE; 83105964.

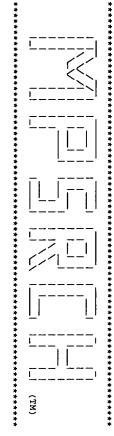
WEAVER C.A., GORDON D.F., KEMPER B.;

MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 32-115.

MEDLINE; 71076162.

MILLL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS
AURBACH G.D., POTTS J.T. JR.;
AURPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                   CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 32-115.
MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
                                                                                                                            SIGNAL
PROPEP
CHAIN
                                                                                                                                                               PROSITE;
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                          61
                                                 Match 100.0%;
Local Similarity 100.0%;
nes 8; Conservative
              DVHNEVAL 68
                                                                                                                                                                           A24949; A24949.
ITE; PS00335; PARATHYROID; 1.
  DVHNFVAL 8
                                                                                                                                                                 SIGNAL.
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32
106
115
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31
115
106
12980 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KISSIL M.S., MEAD D.A., KEMPER B.;
                                                                                                      MW;
                                                 Score 57; DB 1; L
Pred. No. 8.14e-03;
0; Mismatches 0
                                                                                                   PARATHYROID HORMONE
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                      67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAJZOUB J.A., NATHANS J., SHARP P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOGAN M.L., DAWSON
                                                                             Length 115;
                                                       0;
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                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTTS J.T. JR.,
                                                                                                                                                                                                                                                                                                                     THE SALTS IN
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                                                       0
                                                       Gaps
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Search completed: Thu Jul 30 10:53:13 1998 Job time : 6 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:53:31 1998; MasPar time 3.69 Seconds 91.336 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-24 (1-8) from US08817547A.pep 57 1 DVHNFVAL 8

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.944; Variance 25.449; scale 0.862

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Naudalaaa	Result
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444444444444444444444444444444444444444	Score
800 7780 7780 7780 7770 7770 7770 7770	9 Query Match
620 105 5525 5525 2505 2505 2505 2505 250	Length
110000000000000000000000000000000000000	8G 1
001909 063473 995793 006642 063577 016702 028710 0221158 0247723 013290 02113290 02113290 02113291 0213291 0213291 0213291 021344 018266 092566 092566 092566 092566 094770 039628	Ħ
SIMILARITY TO MULTIPLE PARATHYROID HORMONE (F STBA.  PUTATIVE FLAGELLA-RELA FATTY ACID SYNTHASE. (E GENOME, PARTIAL SEQUEN HYPOTHETICAL 15.7 KD P SIMILAR TO S. CEREVISI HYPOTHETICAL 49.1 KD P SIMILAR TO MULTIDRUG-R ERCC2/XPD.  EXC2/XPD.  EXC2/XPD.  EXC2/XPD.  EXC2/XPD.  EXC2/XPD.  EXC2/XPD.  EXC2/XPD.  EXC2/XPD.  EXC30.6 PROTEIN.  K08E7.5.  SIMILAR TO MULTIDRUG-R MYELOBLAST KIAA0279 (F FROM BASES 2775730 TO ABC TRANSPORTER (OLICO CYCLOPHILIN HOMOLOG TA ORF36L.	
1.28e+01 2.08e+01 2.08e+01 2.08e+01 2.08e+01 2.08e+01 3.35e+01 5.35e+01 5.35e+01 5.35e+01 6.47e+01 8.47e+01 8.47e+01	Pred. No.

7. 224 9 P/8229 ALPHA-RAYLASE (EC. 3. 24. 21. 21. 21. 21. 21. 22. 21. 21. 21. 21	41	41	41	41	41	41	41	41	41	41	35 41 71	42	42	42	42	42	42		42	42	42		42	42	4.2
3 094311 1 008726 9 093862 10 p97869 3 018153 9 p95169 8 p93479 1 001437 1 001437 3 021149 4 005261 1 9 p95962 3 021178 3 0118285 3 0123315 3 023315		6.	.0	.9	٠,	٠	٠	•	•	•	. 6	. 7	. 7	. 7	. 7	. 7	. 7	. 7	. 7	. 7	. 7	. 7	. 7	. 7	. '
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ALHHA-AMYLASE (EC 3.2. SIMILARITY TO EGF-LIKE CHROMOSOME XV READING CHROMOSOME XV READING MICROSOMAL EPOXIDE HYD COSMID C25E10. CYCLIN. NUOM (FRAGMENT). BERBERINE BRIDGE ENZYM YELLOW. ACETYL-COA SYNTHETASE. SODIUM/POTASSIUM ATPAS SODIUM/POTASSIUM ATPAS (88E7, 9. PHOSPHATIDYLINOSITOL 4 ORF C04023. ZK1010.6. T27A1.2 PROTEIN. SIMILAR TO K12H4.7 AND F44F1.5. CHROMOSOME XV READING ZC434.5. BAI 1. BAI 2. BAI 1. BAI 1. BAI 1. BAI 1.	Q09515	Q93637	Q93636	014514	Q23315	Q08491	002261	018198	017273	018285	P95962	002811	Q21349	Q27766	Q01576	002437	P93479	P95169	Q40223	Q18153	P97869	Q53662	208726	094311	ç
		F29G6.3A.	F29G6.3B.	$\mathbf{-}$	2C434.5.	۷Χ	F44F1.5.	TO K12H4.7		2K1010.6.	ORF C04023.		K08E7.9.	SODIUM/POTASSIUM ATPAS	SYNTHETASE	YELLOW.	E	NUOM (FRAGMENT).	CYCLIN.	COSMID C25E10.	EPOXIDE		۷Χ	TO	(EC

Ф	M B O	SORERE	RRRRR	R R R R	RRA RRA RRA	RESULT AC ODT ODT ODT ODT OC OC OC OC E OC OC E OC
134 DVHREVIL 141	Query Match 80.7%; Score 46; DB 3; Length 620; Best Local Similarity 75.0%; Pred. No. 1.28e+01; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	SEQUENCE FROM N.A. STRAIN-BRISTOL N2; WATERSTON R.; WATERSTON R.; SUBMITTED (MAX-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF003388; G2088851; EMBL; AF003388; G2088851; SEQUENCE 620 AA; 67475 MW; 17C581A5 CRC32;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-BRISTOL N2; DU Z., GATTUNG S.; SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	SONNHAMMER E., STADEN R., SULSTON J., AS K., VAUDIN M., VAUGHAN K., WATERSTON R., C., WILKINSON-SPROAT J., WOHLDMAN P.;	SEQUENCE FROM N.A.  SERAIN-BRISTOL NZ;  MEDLINE; 94150718.  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  WILSON R., DERTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L.,  CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  CRAXTON M., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  JONES M., KERSHAW J., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.,  PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,	O01909  O01909  O1-JUL-1997 (TREMBLREL. 04, CREATED) O1-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) O1-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) O1-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) SIMILARITY TO MULTIPLE CADHERIN-TYPE REPEATS. R10F2.2. CAENORHABDITIS ELEGANS. CAENORHABDITIS ELEGANS. EUKARYOTA; METAZOA; ACOSLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.

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1 DVHNFVAL 8

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RESULT

ID Q63473;

C Q63473;

DT Q1-NOV-1996 (TREMBLREL. Q1, CREATED)

DT Q1-NOV-1996 (TREMBLREL. Q1, LAST SEQUENCE UPDATE)

DT Q1-NOV-1998 (TREMBLREL. Q5, LAST ANNOTATION UPDATE)

DT Q1-JAN-1998 (TREMBLREL. Q5, LAST ANNOTATION UPDATE)

DE PARATHYROID HORMONE (FRAGMENT).

GN PTH.

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MACCE UTHERIA; RODENTIA.

RN [1]

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE-THYROID, AND PARATHYROID;

RA SCHMELLZER H.J., GROSS G., MAYER H.;

ADV. GENE TECHNOL. 21:228-229(1984).
Search completed: Thu Jul 30 10:53:58 1998 Job time: 27 secs.
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                                                                                                                                                             В
                                                                                                                                                                                                          Query Match 78.9%; Score 45; DB 10; Length 105; Best Local Similarity 75.0%; Pred. No. 2.08e+01; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-THYROID, AND PARATHYROID;

SCHMELER H.J., GROSS G., MAYER H.;

ADV. GENE TECHNOL. 21:228-229(1984).

EMBL; M54875; G601933; -.

NON_TER 1 1

NON_TER 1 1

SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
[1]
                                                                                                     51 DGHNFVSL 58
| ||||:|
1 DVHNFVAL 8
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:57:17 1998; MasPar time 2.55 Seconds 42.121 Million cell upda

cell updates/sec

abular output not generated

Description: Perfect Score: Title: (1-7) from US08817547A.pep 51 >US-08-817-547A-25

Sequence: VHNFVAL 7

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.130; Variance 42.680; scale 0.354

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

11	esult No.
22222222222222222222222222222222222222	Score
111111111111111111111111111111111111111	Query Match
33 33 33 33 34 44 44 44 44 44 44 44 44 4	Length
000001744444444444444444444444444444444	BG
R58149 R58129 R58129 R5812946 W251946 W251946 W251946 R23227 R2323314 R23279 R23279 R23279 R23279 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23276 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R23384 R2	ij
[Asn21]-hpTH(1-38)-OH [Ais19]-hpTH(1-38)-OH [Asp19]-hpTH(1-38)-OH Human parathyroid hor Fusion protien compri Human parathyroid hor Human parathyroid hor Human parathyroid hor Bovine parathyroid ho Bovine parathyroid ho Porcine parathyroid ho Dovine parathyroid hor Porcine parathyroid hor	Description
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31 vhnfval

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HESULT AND COLOR OF THE COLOR O
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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(BAUE/) BAUER W.
(SANO) SANDOZ PATENT GMBH.
(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
Albert R, Bauer W, Breckenridge R, Card.
Gombert F, Gram H, Lewis I, Ramage P, (Gentli R, Rainer A)
WEI, 94-018352/03.
WEI, 94-018352/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.
                                                                                                                                                            hypoparathyroidism. Sequence 38 AA;
                                                                                                                                                                                                                                   New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 139; Page 40; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB2269176-A.
02-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R58142 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R58142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-SEP-1994 (first entry)
[Asn21]-hPTH(1-38)-OH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
8
    Score 51; DB 9; Length 38; Pred. No. 1.64e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₿
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P, Schneider
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RESULT

20 TYNEYAL /

NO R89129 standard; peptide: 38 AA.

AC R89129 standard; peptide: 38 AA.

AC R89129 standard; peptide: 38 AA.

AC R89129 standard; peptide: bPTH; variant; analogue;

KW Human parathyroid hormone; bPTH; variant; analogue;

KW Human parathyroid hormone; bPTH; variant; analogue;

KW Human parathyroidism.

OS SYNthetto.

OS CORD STANDARD ST
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************************* (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:56:41 1998; MasPar time 3.23 Seconds 79.088 Million cell updates/sec

Pabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-25 (1-7) from US08817547A.pep 51 1 VHNFVAL 7

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.152; Variance 25.908; scale 0.816

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	u	4	ω	N	1	No.
42	<b>4</b> 3	44	45	45	45	45	45	45	46	46	49	51	51	51	51	51	51	51	51	51	51	51	Score
							88.2			•		100.0	100.0	100.0	100.0	100.0	100.0	•	•	100.0	100.0	100.0	Query Match
46	2512	227	2509	2505	2504	2504	687	297	201	136	115	115	115	115	115	37	37	36	35	34	34	34	Length
N	_	N	N	ب	N	N	N	N	N	N	N	Н	_	N	Н	σı	G	σ	ഗ	IJ	σı	Çī	BB
S45724	XYCHFA	S33956	G01880	XYRTFA	A57788	B57788	H64665	S55085	C65188	S73520	A05091	PTBO	PTPG	JC4202	PTHU	12WC	1HPH	1ZWB	1ZWD	1ZWF	1 ZWG	1ZWE	Ħ H
	α.	ubiquitin thiolestera	fatty-acid synthase (	fatty-acid synthase (		fatty-acid synthase (	യ	hypothetical protein	hypothetical 22.3 kD	MG441 homolog E09_orf	hormone	parathyroid hormone p	parathyroid hormone p	hormone	parathyroid hormone p		parathyroid hormone f	٠.		parathyroid hormone 4	parathyroid hormone 4	parathyroid hormone (	Description
5.98e+01		2.41e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	9.40e+00	9.40e+00	2.18e+00		7.97e-01	7.97e-01	7.97e-01	7.97e-01	7.97e-01	7.97e-01	7.97e-01	7.97e-01	7.97e-01	7.97e-01	Pred. No.

45	44	43	42	41	40	39	38	37	36	<u>ω</u>	34	33	32	31	30	29	28	27	26	25
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1520	924	864	632	599	537	672	541	316	216	212	212	208	207	183	182	182	182	182	178	105
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G69634	S34926	S13381	S73824	S18612	S67434	S46276	A25696	S07569	A56861	A40047	A54204	CSHUB	A40516	S71547	2RMCA	2RMCG	2RMCC	2RMCE	1CYNA	I51851
3	hypothetical protein	lipoxygenase (EC 1.13	MG242 homolog H91_orf	lipoxygenase (EC 1.13	hypothetical protein	acetateCoA ligase (	yellow protein - frui	protein H5 - slime mo	peptidylprolyl isomer	Cyclophilin c complex	Cyclophilin c complex	Cyclophilin c complex	Cyclophilin c complex	cyclophilin b, chain	parathyroid hormone -					
9.32e+01	9.32e+01	9.32e+01	•	9.32e+01	9.32e+01		5.98e+01	5.98e+01	5.98e+01			5.98e+01	5.98e+01	5.98e+01						

#Submission submitted to #CTOSS-references PDB:1ZWG REFERENCE TN003319 #Bauthors Marx, U.C. #book in Strukture pp.0, Bayr COMMENT Resolution: not ap	ENTRY TITLE ALTERNATE NAMES POB_TITLE ORGANISM REFERENCE #authors	Best Local Simi Matches 7;  Db 28 VHNFVAL         Qy 1 VHNFVAL	#book  COMMENT Resol COMMENT Deter KEYWORDS FEATURE 15-25 SUMMARY	ALTERNATE_NAMES HPTH(4-37)  PDB_TITLE structure of structures at a formal_name at a formal_name at a formal_structure of submitted to sub	RESULT 1 ENTRY TITLE
the n Ver euth plica	#type complete id hormone 4 37 mutant N-TERMINAL SUCCINYLA l-hpth(4-37) numan parathyroid hormone 4-37, NMR, 10 str ame synthetic ; Marx, U.C.	Best Local Similarity 100.0%; Pred. No. 7.97e-01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 28 VHNFVAL 34        1 VHNFVAL 7	Verschiedener Parath tth: University of B icable licable lelix (right hand alp olecular weight 4128	human F Homo sa Marx, U.	12WE #type complete parathyroid hormone (residues 4-37) - human

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COMMENT

disease mutation; hormone; signal

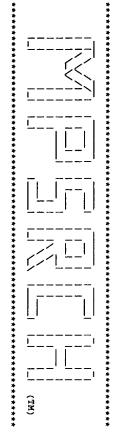
FEATURE
2-9
15-25 #region helix (right hand alpha)\
15-25 #region helix (right hand alpha)\
15-25 #region helix (right hand alpha)\
15-25 #length 34 #molecular-weight 4.128 #checksum 5508

Query Match
Best Local Similarity 100.0%; Score 51; DB 5; Length 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 VHNFVAL 34
Qy 1 VHNFVAL 7

Search completed: Thu Jul 30 10:57:00 1998

Job time: 19 secs.
```



Psrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:55:35 1998; MasPar time 2.08 Seconds 84.457 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-25 (1-7) from US08817547A.pep 51 1 VHNFVAL 7

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.139; Variance 21.222; scale 1.043

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Sult No.	Score	Query Match	Length	BG	IJ	Description	Pred. No.
-	51	100.0	115	ㅁ	PTHY_CANFA	PARATHYROID HORMONE PR	8.19e-02
2	51	100.0	115	Н		HORMONE	8.19e-02
ω	51	100.0	115	μ	PTHY_PIG	PARATHYROID HORMONE PR	•
4	51	100.0	115	μ	PTHY_HUMAN	PARATHYROID HORMONE PR	
5	49	96.1	115	Н	PTHY_RAT	PARATHYROID HORMONE PR	
σ	46	90.2	136	Н	Y441_MYCPN	HYPOTHETICAL PROTEIN M	
7	46	90.2	200	1	YIGP_ECOLI	HYPOTHETICAL 22.3 KD P	1.66e+00
- α	45	88.2	297	,_	YMY9_YEAST	HYPOTHETICAL 34.0 KD P	2.95e+00
. •	45	88.2	687	Н	CSTA_HELPY	CARBON STARVATION PROT	2.95e+00
10	45	88.2	2504	H	FAS_HUMAN	FATTY ACID SYNTHASE (E	
11	45	88.2	2505	<b>ب</b>	FAS_RAT	FATTY ACID SYNTHASE (E	2.95e+00
12	44	86.3	227	μ.	UBL_DROME	UBIQUITIN CARBOXYL-TER	5.18e+00
13	44	86.3	505	۳	Y4XG_RHISN	HYPOTHETICAL 55.5 KD P	5.18e+00
14	43	84.3	752	μ	CUL1_HUMAN	CULLIN HOMOLOG 1 (CUL-	9.02e+00
15	43	84.3	2511	۲	FAS_CHICK	FATTY ACID SYNTHASE (E	9.02e+00
16	42	82.4	161	Ь	YCX5_EUGGR	HYPOTHETICAL 18.6 KD P	1.55e+01
17	42	82.4	207	ب	CYPB_CHICK	PEPTIDYL-PROLYL CIS-TR	1.55e+01
18	42	•	208	Н	CYPB_RAT	PEPTIDYL-PROLYL CIS-TR	1.55e+01
19	42	82.4	208	μ	CYPB_HUMAN	PEPTIDYL-PROLYL CIS-TR	1.55e+01
20	42	82.4	208	H	CYPB_MOUSE	PEPTIDYL-PROLYL CIS-TR	1.55e+01
21	42	•	208	ш	CYPB_BOVIN	PEPTIDYL-PROLYL CIS-TR	1.55e+01
22	42	•	212	ш	CYPC_HUMAN	PEPTIDYL-PROLYL CIS-TR	1.55e+01
23	42	82.4	212	Н	CYPC_MOUSE	PEPTIDYL-PROLYL CIS-TR	1.55e+01

42 82.4 541 1 YELL_ROME YELLOW PROTEIN. 41 80.4 537 1 AREH_SCHPO PROBABLE STEROL O-ACYL 41 80.4 632 1 Y242_MYCPN HYPOTHETICAL PROTEIN M 41 80.4 864 1 LOXX_SOYBN SEED LIPOXYGENASE (EC 41 80.4 924 1 Y853_YEAST HYPOTHETICAL 104.5 KD 40 78.4 216 1 Y856_RAEEL HYPOTHETICAL 104.5 KD 40 78.4 274 1 CDL_SYLFL T-CELL SURFACE GLYCOPR 40 78.4 408 1 GPT_CRIGR UDP-N-ACETYLGLUCOSAMIN 40 78.4 430 1 BMP7_MOUSE BONE MORPHOGENETIC PRO 40 78.4 430 1 BMP7_HUMAN BONE MORPHOGENETIC PRO 40 78.4 431 1 MP7_HUMAN BONE MORPHOGENETIC PRO 40 78.4 507 1 LCK_CHICK PROTO-ONCOGENE TYROSIN 40 78.4 578 1 YFAA_ECOLI HYPOTHETICAL 64.5 KD 40 78.4 782 1 ZFYZ_MOUSE ZINC FINGER Y-CHROMOSO 40 78.4 805 1 ZFYZ_HUMAN ZINC FINGER Y-CHROMOSO 40 78.4 805 1 ZFYZ_HUMAN ZINC FINGER Y-CHROMOSO 40 78.4 805 1 ZFYZ_HUMAN ZINC FINGER Y-CHROMOSO 40 78.4 805 1 SECÉ_YEAST EXCCYST COMPLEX COMPONO 40 78.4 805 1 SECÉ_YEAST EXCCYST COMPONENCING	45	44	43	42	41	40	39	3 8	37	36	<u>3</u> 5	34	33	32	31	30	29	28	27	26	25	4
.4 541 YELL_DROWE .4 537 1 AREH_SCHPO .4 632 1 Y242_MYCPN .4 864 1 LOXX_SOYBN .4 924 1 Y353_YEAST .4 274 1 CDL_SYLFL .4 408 1 GPT_CRIGR .4 408 1 GPT_CRIGR .4 408 1 GPT_CRIGR .4 400 1 BMPT_HUMAN .4 430 1 BMPT_HUMAN .4 430 1 BMPT_HUMAN .4 430 1 GPT_CULI .4 430 1 BMPT_HUMAN .4 430 1 GPT_CHUMAN .4 430 1 GPT_SOLTU .4 782 1 YFAA_ECOLI .4 578 1 YFAA_ECOLI .4 607 1 YFAA_ECOL	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	41	41	41	41	42	4.6
1 YELL_DROME 1 AREH_SCHPO 1 Y242_MYCPN 1 LOXX_SOYBN 1 LOXX_SOYBN 1 LOXX_SYLFL 1 CDL_SYLFL 1 CDL_SYLFL 1 GPT_CRIGR 1 GPT_CRIGR 1 GPT_HUMAN 1 CADB_ECOLI 1 CCADB_ECOLI 1 CCADB_ECOLI 1 LOX_CHICK 1 YFAA_ECOLI 1 LOX_CHICK 1 YFAA_ECOLI 1 ZFYL_MOUSE 1 ZFYL_MOUSE 1 ZFYL_MOUSE 1 ZFYL_MOUSE 1 ZFYL_HUMAN 1 ZEG_YEAST 1 ENV_EVIW2 1 TENT_HUMAN 1 ZEG_YEAST 1 ENV_EVIW2	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	80.4	80.4	80.4	80.4	82.4	
YELL_DROME AREH_SCHPO Y242_MYCPN LOXX_SOYBN LOXX_SOYBN LOXX_SOYBN YB53_YEAST YS6_CAEEL CDL_SYLFT CRIGR GPT_CRIGR GPT_CRIGR GPT_HUMAN CADB_ECOLI LCK_CHICK YFAA_ECOLI USST_SOLTU ZFYL_MOUSE ZFY2_MOUSE ZFY2_HUMAN SEC6_YEASN SEC6_YEASN SEC6_YEASN SEC6_YEASN SEC6_YEASN SEC6_YEASN SEC6_YEASN	847	805	805	801	783	782	607	578	507	444	431	430	408	408	274	216	924	864	632	537	541	
	_	ب	_	_	۳	<b>ب</b>	Н	μ	۱	<u>ب</u>	μ	Н	<b>ب</b> ــو	_	Н	<u>_</u>	ب	_	Н	بر	ب	,
YELLOW PROTEIN.  YELLOW PROTEIN.  PROBABLE STEROL O-ACYL HYPOTHETICAL PROTEIN M SEED LIPOXYGENASE (EC HYPOTHETICAL 104.5 KD HYPOTHETICAL 104.5 KD HYPOTHETICAL 23.9 KD T-CELL SURFACE GLYCOPR UDP-N-ACETYLGLUCOSAMIN BONE MORPHOGENETIC PRO BONE MORPHOGENET	ENV_HV1W2	SEC6_YEAST	ZFX_HUMAN	ZFY_HUMAN	ZFY2_MOUSE	ZFY1_MOUSE	UGST_SOLTU	YFAA_ECOLI	LCK_CHICK	CADB_ECOLI	BMP7_HUMAN	BMP7_MOUSE	GPT_CRILO	GPT_CRIGR	CD1_SYLFL	YS86_CAEEL	YB53_YEAST	LOXX_SOYBN	Y242_MYCPN	AREH_SCHPO	YELL_DROME	10101010
	ENVELOPE POLYPROTEIN G	EXOCYST COMPLEX COMPON	FINGER	FINGER	FINGER		GRANULE-BOUND GLYCOGEN	HYPOTHETICAL 64.5 KD P	PROTO-ONCOGENE TYROSIN	PROBABLE CADAVERINE/LY	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	UDP-N-ACETYLGLUCOSAMIN	UDP-N-ACETYLGLUCOSAMIN	T-CELL SURFACE GLYCOPR		HYPOTHETICAL 104.5 KD			PROBABLE STEROL O-ACYL	YELLOW PROTEIN.	***

888	2 5	Z C	ij	DI	AC	ID	RESULT	Qγ	В	M	å ö	SQ	ΗŢ	ΕŢ	ΕŢ	ΧW	DR	DR	ဌ	റ്റ	R.	RA :	RA :	₹ ?	5 7		8	8	SO	GN	DE	ΡŢ	Ŋ	ដ្ឋ	ð	Ħ	RESULT
TAURUS RYOTA;	PTH HOLD HOLDING	(KEL.	(REL.	21-JUL-1986 (REL.		PTHY_BOVIN STA	2	1 VHNFVAL 7	62 VHNEVAL 68	nes 7;	Query Match Best Local Similarity	SEQUENCE 115 AA;	CHAIN 32			SIGNAL.	PROSITE; PS00335;			- I - FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING	GENE 160:241-243(1995).	DEWILLE J.W., CAPEN C.C.;	ROSOL T.J., STEINM	MEDLINE: 95369696.	TICCHE BARATHYROID	[1]	EUTHERIA; CARNIVORA.	EUKARYOTA; METAZOA;	CANIS FAMILIARIS (DOG)				(REL	(REL.	ົ້ວ	THY CANFA	OLT 1
(BOVINE). METAZOA; CHORDATA; VE		U	01, LAST SEQUENCE	CREA		STANDARD; PF				rvative	100.0%; Score 100.0%; Pred.	957 MW;			25 BY			916;	PREVENTING THEIR RENAL	ELEVATES CALCI	995).			•	•		Α.	CHORDATA;	•		RECUR	34, LAST ANNOT		34, CREATED)		STANDARD; PF	
VERTEBRATA; TET	FRECONOCK (FRANCILINIA) (FIA)	LAST ANNOTATION OPDATE)	ENCE UPDATE)			PRT; 115 AA.	,			Misma	e 51; DB 1; L 1. No. 8.19e-02;	16ED0EBC CRC32;	PARATHYROID HORMONE	SIMILARITY.	SIMILARITY.		•		CNAL EXCRETION.	OM LEVEL BY D		!	MCCAULEY L.K., G					VERTEBRATA; TET			ARATHYRIN) (P		NCE UPDATE)			PRT; 115 AA.	
TETRAPODA; MAMMALIA;	111).	30,								; Indels	Length 115; 2;	••	ONE.							ISSOLVING THE			GRONE A.,					TETRAPODA; MAMMALIA;			TH).						
ΙΑ;										0; Gaps 0;										SALTS IN								IA;									

SEQUENCE FROM N.A.
MEDLINE; 82037785.
WEAVER C.A., GORDON D.F.,
PROC. NATL. ACAD. SCI. U.S

F., KEMPER B.; U.S.A. 78:4073-4077(1981).

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A., POTTS J.T. JR., RICH A.; PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).

SEQUENCE FROM N.A. MEDLINE; 80056617. EUTHERIA; ARTIODACTYLA.

80056617

SEQUENCE FROM N.A.

MEDLINE; 83105964.

WEAVER C.A., GORDON D.F., KEMPER B.;

MOL. CELL. ENDOCRINOL. 28:411-424(1982).

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DR CCCCRARAR RELEASE R
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                                                            В
                                                                                                                                                                                                                                                SQ ST
                                                                                                                     Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 71091588.

MEDLINE; 71091588.

POOTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

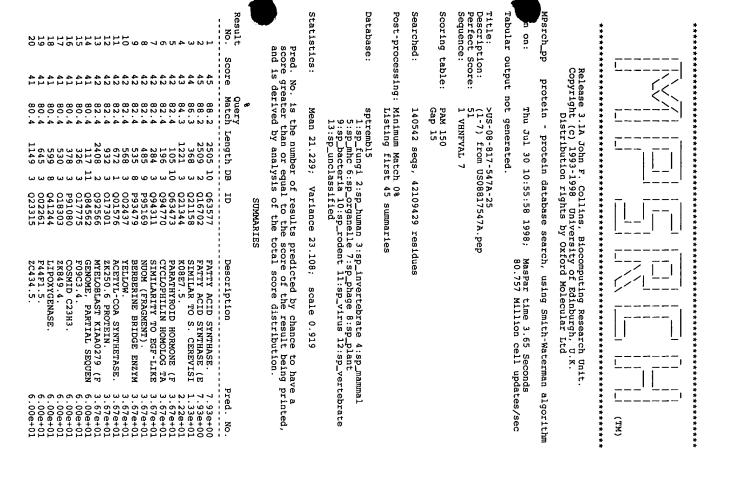
-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; V00023; G163641; -.
EMBL; V00024; G163643; -.
EMBL; J00024; G163643; ALT_INIT.
EMBL; M01938; G163647; -.
EMBL; N01938; G163647; -.
EMBL; M01938; G163645; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 32-115.

MEDILINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS
AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T.,
                                                                                                                                                                                                                                             CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 32-115.
MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                              HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A01534; PTBO.
PIR; A24949; A24949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHESIS OF 32-65.
                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00335; PARATHYROID; 1.
                                                               62 VHNFVAL 68
      1 VHNFVAL 7
                                                                                                              h 100.0%;
Similarity 100.0%;
7; Conservative
                                                                                                                                                                                                                                                106
115 AA;
                                                                                                                                                                                                                                             25
31
115
P
106
V
12980 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KISSIL M.S., MEAD D.A., KEMPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
?
                                                                                                                        Score 51; DB 1; Length 115;
Pred. No. 8.19e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                             PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOGAN M.L., DAWSON B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTTS J.T. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B.
                                                                                                                                 0
                                                                                                                                 Gaps
                                                                                                                                 0;
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Search completed: Thu Jul 30 10:55:41 1998 Job time: 6 secs.



41 80.4 17/4 3 9335 FXSP FAST STEEL INVOLVED 41 80.4 19:8 3 93637 F2966.3A.  40 78.4 90 11 Q72852 ENVELOPE GLYCOPROTEIN 40 78.4 91 11 Q72856 ENVELOPE GLYCOPROTEIN 40 78.4 115.5 P77949 CYCLOPHILIN SCCYPB (EC 40 78.4 256 6 Q33000 CNF115.5 CYCLOPHILIN SCCYPB (EC 40 78.4 256 6 Q33000 FATE CONTROL 20.0 KD P 78.4 256 6 Q33000 FATE CONTROL 20.0 KD P 78.4 400 2 Q15216 GLYCOPTEIN 21 PRECURSOR. 40 78.4 400 2 Q15210 GLYCONTE PRECURSOR. 40 78.4 400 2 Q15110 GLYCONTE PRECURSOR. 40 78.4 601 9 Q07176 GLYCONTE PRECURSOR. 40 78.4 601 9 Q07176 HYPOTHETICAL 68.6 KD P 78.4 659 3 Q18406 CODED FOR BY C. ELEGAN 40 78.4 851 11 Q71819 Y48EJB.5. 40 78.4 861 11 Q71819 GLYCOPROTEIN 40 78.4 862 11 Q71819 ENVELOPE GLYCOPROTEIN 40 78.4 862 11 Q73336 ENVELOPE POLYPROTEIN. 40 78.4 1113 2 Q15056 KIAAO348.
4 1/74 3 093637 F2966.3A. 4 1913 1 PR7204 FXSP PROTEIN: 4 1918 3 093637 F2966.3A. 4 99 11 072849 ENVELOPE GLYCC 4 91 11 072852 ENVELOPE GLYCC 4 91 11 072854 ENVELOPE GLYCC 5 115 6 033000 CNF115: 6 034000 CNF115: 7 9 P77949 CYCLOPHILIN S. 7 256 6 004315 HYPOTHETICAL: 7 296 9 P76472 FROM BASES 2A. 7 296 9 P76472 FROM BASES 2A. 7 296 9 P71364 GLCNAC-1-P TR. 7 4 460 9 051510 PROTEIN E1 PR. 7 4 460 9 07156 GLCNAC-1-P TR. 7 601 9 007176 PROTEIN E1 PR. 7 601 9 007176 HYPOTHETICAL: 7 601 9 007176 HYPOTHETICAL: 7 601 9 007176 GLCNAC-1-P TR. 7 601 9
1 P87204 FXSP PROTEIN: 1 P87204 FXSP PROTEIN: 1 072849 ENVELOPE GLYCC 11 072852 ENVELOPE GLYCC 11 072856 ENVELOPE GLYCC 11 072856 ENVELOPE GLYCC 11 072854 ENVELOPE GLYCC 11 072854 ENVELOPE GLYCC 10 073000 ORF115: 10 0733049 CYCLOPHILIN SI 10 074315 FROM BASES 23: 19 P76472 FROM BASES 23: 2 015216 GLCNAC-1-P TR 19 P76364 GLCNACE-1-P TR 19 P76364 GLCNATE PER 19 P76364 GLUCONATE PER 19 P76364 GLUCONATE PER 19 P76364 GLUCONATE DER 19 P76472 GLUCONATE DER 19 P76472 GLUCONATE DER 19 P76472 GLUCONATE DER 10 076472 GLUCONATE DER 10 0764
1 P87204 FXSP PROTEIN: 1 P87204 FXSP PROTEIN: 3 Q93637 F2966.3A. 11 Q772849 ENVELOPE GLYCC 11 Q772852 ENVELOPE GLYCC 11 Q772854 ENVELOPE GLYCC 12 Q33000 CYCLOPHILIN SI 15 Q033010 CYCLOPHILIN SI 16 Q04315 HYPOTHETICAL: 17 Q76315 GLYCCATE PROM BASES 23: 18 Q051510 FROM BASES 23: 18 Q051510 FROM BASES 23: 18 Q051510 FROM BASES 23: 2 Q15516 GLYCANC-1-P TR. 19 Q51510 FROM BASES 23: 2 Q15516 GLYCANC-1-P TR. 19 Q07176 GLYCOPHOTICAL: 3 Q18406 COSMID F35D2. 3 Q18406 COSMID F35D2. 3 Q15558 TESTIS DETERM. 11 Q41593 ENVELOPE GLYCC 11 Q773336 ENVELOPE GLYCC 2 Q15556 KIAA0348.
FY9G6.3A.  FKSP PROTEIN:  7 F29G6.3A.  9 ENVELOPE GLYCC  2 ENVELOPE GLYCC  4 ENVELOPE GLYCC  4 ORF115.  CYCLOPHLIN SI  HYPOTHETICAL:  2 FROM BASES 23:  FROM BASES 23:  GLCUAC-1-P TR.  PROTEIN E1 PR.  GLUCONATE PR.  GLUCONATE PR.  SIMILAR TO.  SIMILAR TO.  SIMILAR TO.  SIMILAR TO.  SIMILAR TO.  CODED FOR BY OR B
PROTEIN: 6.3A. LOPE GLYCO LOPE GLYCO LOPE GLYCO LOPE GLYCO 15. BASES 2A: THETICAL P TR. BASES 2A: THETICAL LARITY TO THETICAL ILARITY TO THETICAL IN E1 PRI OTHETICAL

#### PIGNMENTS

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RESULTA

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RESULT
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Best Local S
Matches
                    O16702
Q16702
Q16702
Q16702;
O1-NOV-1996 (TREMBLREL. O1, CREATED)
O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE UPDATE)
O1-JAN-1998 (TREMBLREL. O5, LAST ANNOTATION UPDATE)
FATTY ACID SYNTHASE (EC 2.3.1.85) (FATTY-ACID SYNTHASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 1

PRELIMINARY; PRT; 2505 AA. 063577

O1-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UF 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION FATTY ACID SYNTHASE.
RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE; 92141210.

SMITH S., NAGGERT J., WILLIAMS-AHLE B.,

PROC. NATL. ACAD SCI. U.S.A. 89:1105-1

PROS. M84761; G204099; -

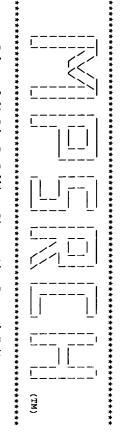
PROS. TE; PS00012; PHOSPHOPANTETHEINE; PROS. TE; PS00012; PHOSPHOPANTETHEINE; PROS. TE; PS00606; B_KETOACYL_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 89240686.
AMY C.M., WITKOWSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
   HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROC. NATL. ACAD. SCI. U.S.A. 86:3114-3118(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMITH S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                             550 VHSFVSL 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                  VHNFVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272663 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILLIAMS-AHLF B., AMY C.M.; U.S.A. 89:1105-1108(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAGGERT J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 10;
Pred. No. 7.93e+00;
2; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5151416A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILLIAMS B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANDHAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.

RN [1]
RP SEQUENCE FROM N.A.
RA HENNIGAR R.A., JENNER K.H., HEINE H.S., KAYLER A.E., WOOD F.D.,
RA HENNIGAR R.A., JENNER K.H., HEINE H.S., KAYLER A.E., WOOD F.D.,
RA KUHAJDA F.P., PASTERNACK G.R.;
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + MALONYL-COA + 2N NADPH = A
CC LONG-CHALN FATTY ACID + (N+1) COA + N CO(2) + 2N NADPH = A
CC EMBL; U29344; G915392; -.
DR PROSITE; PSO00612; PHOSPHOPANTETHEINE; 1.
DR PROSITE; PSO00615; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PSO06615; B_KETOACYL_SYNTHASE; 1.
KW TRANSFERASE.
SQ SEQUENCE 2509 AA; 273089 MW; D1E74B76 CRC32;
QUETY MATCh
B8.2%; Score 45; DB 2; Length 2509;
Best Local Similarity 71.4%; Pred. No. 7.93e+00;
Best Local Similarity 71.4%; Pred. No. 7.93e+00;
MATChes 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
MATCHES 550 VHSFVSL 556
1 VHNFVAL 7

Search completed: Thu Jul 30 10:56:24 1998

Job time: 26 secs.
```



srch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:59:44 1998; MasPar time 2.58 Seconds 35.687 Million cell updates/sec

Tabular output not generated.

Perfect Score: Title: Description: (1-6) from 44 1 HNFVAL 6 >US-08-817-547A-26 (1-6) from US08817547A.pep

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.505; Variance 37.183; scale 0.390

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
44444444444444444444444444444444444444	Score
1000.000.0000.000000000000000000000000	% Query Match
C C C C C C C C C C C C C C C C C C C	Length
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	BB
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[Asn21]-hPTH(1-38)-OH [His19]-hPTH(1-38)-OH [His19]-hPTH(1-38)-OH [Asp19]-hPTH(1-38)-OH [Asp19]-hPTH(1-38)-OH Human parathyroid hor Fusion protien compri Human parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Porcine parathyroid hor Porcine parathyroid hor Porcine parathyroid hor Fundan parathyroid hor Porcine parathyroid hor Fundan parathyroid hor Human parathyroid hor Human parathyroid hor Human parathyroid hor Human parathyroid hor	Description
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R23449	121	121	R23363	R23456	R23240	R23374	R23433	R23392	R21238	R21234	R21181	R23227	R21187	R21219	R21250	R23248	R29561	R29562	W29420	R21240	R21241	σ	16	R23383	4
ne parathyroi	Human parathyroid hor	Human parathyroid hor	Bovine parathyroid ho	Ò.	Human parathyroid hor	Bovine parathyroid ho	0	à	Human parathyroid hor	įd	Human parathyroid hor	Human parathyroid hor	Oxidation resistant P	Oxidation resistant [	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	ant	Human parathyroid hor	Porcine parathyroid h	ċ				
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В
                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                        12-JUL-1993; 014384.

15-JUL-1992; GB-026415.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026869.

23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.
                                                                       New active parathyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 139; Page 40; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism.

Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [Asn21]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant;
calcium; depletion; fixation; resorption;
hypoparathyroidism.
                                                                                                                                                                                                Albert R, Bauer W, Breckenridge R, Cardinaux F; Gombert F, Gram H, Lewis I, Ramage P, Schneider Waelchli R, Rainer A; WPI: 94-018352/03
                                                                                                                                                                                                                                                      (SANO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R58142 standard;
R58142;
20-SEP-1994 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1994.
                                                                                                                                                                                                                                                                                (SANO ) SANDOZ
(BAUE/) BAUER V
32 hnfval 37
                                                                                                                                                                                                                                                    SANDOZ-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                  BAUER W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                             LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide;
                       Score 44; DB 9; I
Pred. No. 4.86e+01;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analogue;
osteopathy; osteoporosis;
                          0
                                               Length 38;
                          Indels
                                                                                                                                                                                                                            Η;
                          0
                                                                                                                                  bone
                          Gaps
                          0
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RESULT

2
RESULT

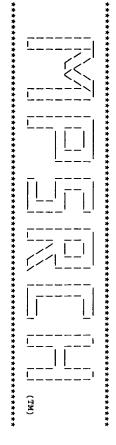
2
RESULT

20-SEP-1994 (first entry)
DE [Phe21]-hPH(1-38)-08.

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis; KW hypoparathyroidism.

Synthetic.

OS Synthetic.
Synt
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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:59:09 1998; MasPar time 3.02 Seconds 72.657 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-26 (1-6) from US08817547A.pep 44 1 HNEVAL 6

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.121; Variance 22.615; scale 0.890

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 5 5 5 5 5 5 5 7 6 6 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	No.
44444444444444444444444444444444444444	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query
34 34 35 35 36 37 37 37 37 115 115 115 115 115 115 115 115 115 11	Length I
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12WE 12WG 12WG 12WG 11ZWD 11ZWD 11EWH 11EWC 1744202 171851 1744200 1751851 1744200 1751851 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 174420 17	Ħ
parathyroid hormone ( parathyroid hormone 4 parathyroid hormone ( parathyroid hormone poreteln protein in hypothetical protesmi UDP-N-acetylglucosami UDP-N-acetylglucosami osteogenic protein 1 bone morphogenetic prorotein 1 bone morphogenetic prorotein 1 protein tyrosine kina yfak protein - Escher threonine - tRNA ligas hypothetical protein	Description
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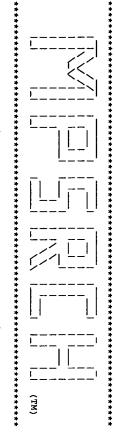
45	44	43	42	41	40	<b>ω</b>	38	37	36	<b>ω</b>	34	33	32	31	30	29	28	27	26	25	24
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A57788	E69121	S66993	A49626	G69593	A42363	G69287	S04110	S67660	JN0878	S72497	S68161	A56163	S43297	140811	B65598	S33956	S39966	JC5638	C65188	S73520	A60776
fatty-acid synthase (	conserved hypothetica	hypothetical protein	transregulatory prote	endo-1,4-beta-glucana	peptidase T - Salmone	hypothetical protein	ťΩ	hypothetical protein	100K protein - fowl a	oligopeptide transpor	oligopeptide transpor	peptide transport pro	oligopeptide transpor	uroporphyrinogen-III	maturation of the out	ubiquitin thiolestera	hypothetical protein	pH-sensing regulatory	hypothetical 22.3 kD	MG441 homolog E09_orf	230k bullous pemphigo
1.24e+02	1.24e+02	1.24e+02	1.24e+02	1.24e+02	1.24e+02	1.24e+02	1.24e+02	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	4.76e+01

#SUBMISSION SUBMITTED TO THE PROPERTY OF THE P	δi	Simil 6; VAL 3 !!! VAL 6	COMMENT Resoluti COMMENT Determin KEYWORDS ho FEATURE 15-25 SUMMARY #1	#Authors Roes #submission submission submiss	1 _NAMES
the n Ver euth plica	#type complete nthetic ccinyl-hpth(4-37) mal_name synthetic ds, P.; Marx, U.C.	100.0%; Pred. No. 6.34e+00 vative 0; Mismatches		A6 /860 P.; Marx, U.C. Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 ces PDB:1ZWE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	1ZWE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man

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COMMENT
COMMENT
CHAPTER

REWORDS

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

92: Thu Jul 30 10:57:48 1998; MasPar time 2.03 Seconds 74.131 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-26 (1-6) from US08817547A.pep 44 1 HNFVAL 6

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.045; Variance 18.682; scale 1.127

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

22222223333444323232222233333433432323232333333	wlt No.
34444444444444444444444444444444444444	Score
1000.00 1000.00 888888888899999999999999999999999	Query Match
115 115 115 115 115 115 115 115 115 115	Length
<u> </u>	DB
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BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	PHH.	( XEL. 50	(ABL. OL)	OI, CREATED)	1551 01	C. C	YHY	JLT 2	1 HNEVAL 6	63 HNEVAL 68	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 100.0%; Score 44; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 1.12e+00;	NCE 115 AA; 12957 MW;	32 115	26	1 25		PROSITE; PS00335; PARATHYROID; 1.	EMBL; U15662; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION	-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN	GENE 160:241-243(1995).		ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE; 95369696.		SEQUENCE FROM N.A.		And the state of t	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:	CANTS FAMILIADIS (DOG)	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).	(REL. 34, LAST ANI	(REL. 34,	01-OCT-1996 (REL. 34, CREATED)		PTHY CANFA STANDARD: PRT: 115 AA.	ILT 1

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Best Local S
Matches
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EMBL; J00023; G163641; --
EMBL; J00024; G163643; --
EMBL; J00024; E18249; ALT_SEQ.
EMBL; J00024; E18250; ALT_INIT.
EMBL; M01938; G163647; --
EMBL; M25082; G163645; --
PIR; A01534; PTBO
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SEQUENCE
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HORMONE;
SIGNAL
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MEDLINE; 84262483.

WEAVER C.A., GORDON D.F., F
GENE 28:319-329(1984).
[5]
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MEDLLNE; 71091588.

POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,

DETTOS L.J., DAWGON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

BONE AND PREVENTING THEIR RENAL EXCRETION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 32-115.

MEDLINE; 71063634.

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MEDLINE; 82037785.
WEAVER C.A., GORDON
PROC. NATL. ACAD. SI
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MEDLINE; 71076162.
MIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS:
AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., COHN D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
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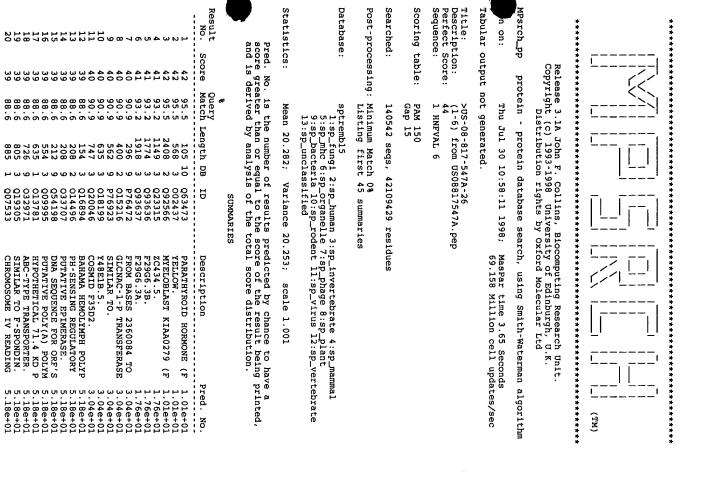
MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
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MEDLINE; 83105964.
MEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                           63 HNFVAL 68
                                                                                      Y Match 100.0%;
Local Similarity 100.0%;
les 6; Conservative
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A24949; A24949.
SITE; PS00335; PARATHYROID;
HNFVAL 6
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115 AA;
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ACAD. SCI. U.S.A. 78:4073-4077(1981).
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Pred. No. 1.12e+00;
0; Mismatches 0;
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                                                                                                                              Length 115;
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Total Control
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:02:08 1998;

Tabular output not generated 8 :: MasPar time 2.54 Seconds 30.164 Million cell updates/sec

Perfect Score: Description: Title: >US-08-817-547A-27 (1-5) from US08817547A.pep 35 1 NEVAL 5

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.768; Variance 32.782; scale 0.420

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3.36e+02	3.36e+02	Pred. No																	

Query Match

100.0%;

Score 35;

DB 9;

Length 38;

4 R21161 Human 25 W29420 Human 25 W29562 Oxida 5 R29562 Oxida 4 R23346 Porci 4 R23346 Human 4 R23346 Human 4 R23379 Bovin 4 R23379 Bovin 4 R23379 Bovin 4 R23336 Bovin 4 R23336 Bovin 4 R23336 Bovin 4 R23338 Forci 4 R23338 Forci 4 R23338 Forci 4 R23175 Human 4 R21174 Human 4 R21174 Human 4 R21211 Human 5 R29563 Human 6 R21211 Oxida 7 R21211 Oxida 8 R21669 Mouse 5 W23060 Mouse 5 W23061 Mouse 5 W23061 Mouse	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANO) SANDOZ LTD.

(BAUE/) BAUER W.

(SANO) SANDOZ PATENT GMBH.

(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

(SANO) SANDOZ LTD.

(SANO) SANDOZ 
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R58019;
20-SEP-1994 (first entry)
N-alpha-methy/[Alal] parathyroid hormone(1-38).
Human parathyroid hormone; hPTH; variant; analogue;
calcium, depletion; fixation; resorption; osteopathy; osteoporosis;
New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 4; Page 34; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism.

Sequence 38 AA;
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Ser residue at position 1"
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12-UUL-1993; GB-015009.

112-UUL-1992; GB-015009.

115-UUL-1992; GB-026415.

18-DEC-1992; GB-02645.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-001691.

PR 23-DEC-1992; GB-001691.

PR 14-APR-1993; GB-001691.

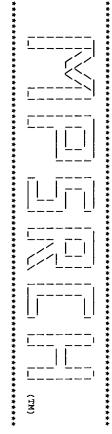
PR 14-APR-1993; GB-001692.

PR 14-APR-1993; GB-001692.

PR 14-APR-1993; GB-00033.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ PATENT GMBH.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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[Alai9]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
hypoparathyroidism.
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R58126 standard; peptide; 38
R58126;
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                                           Jul 30 11:02:23 1998
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0; Mismatches 0;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:01:26 1998; MasPar time 3.08 Seconds 59.234 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-27 (1-5) from US08817547A.pep 35 1 NEVAL 5

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 19.157; Variance 19.754; scale 0.970

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

22222000000000000000000000000000000000	No.
	Score
	Match
34 34 34 35 35 36 37 37 37 37 37 115 115 115 118 218 218 218 220 200 200	Match Length
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1ZWF 1ZWG 1ZWG 1ZWB 1ZWD 1ZWD 1ZWD 1ZWD 1ZWC 845724 821218 9TB0 9TB0 9TB0 9TB0 9TB0 9TB0 9TB0 9TB0	IB
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(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:00:15 1998; MasPar time 2.01 Seconds 62.409 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-27 (1-5) from US08817547A.pep 35

Description: Perfect Score: Sequence: 1 NEVAL 5

Scoring table:

PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 20.019; Variance 16.358; scale 1.224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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POLYP	BUD SITE SELECTION PRO	PUTATIVE DNA POLYMERAS	OUTER CAPSID PROTEIN V	PLATELET ENDOTHELIAL C	HYPOTHETICAL 80.1 KD P	DNA PRIMASE (EC 2.7.7.	HYPOTHETICAL 65.9 KD P	PUTATIVE GLUTAMATE DEC	YELLOW PROTEIN.	HYPOTHETICAL 59.7 KD P	ENDOPLASMIC RETICULUM	PROTEIN DISULFIDE ISOM	PRE-B CELL ENHANCING F	REPLICATIVE DNA HELICA	PROBABLE CADAVERINE/LY	RF4 PROTEIN.	N-ACETYLGLUCOSAMINYLTR	ALPHA-LYTIC PROTEASE P	MATRIX PROTEIN.	MATRIX PROTEIN.	HYPOTHETICAL 32.9 KD P
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MEDLINE: 73227467.

ANDREATTA R.H., HARTMANN A., JOEHL A.,
RINKER B., RITTEL W., SIEBER P.;
RINKER B., RITTEL W., SIEBER P.;
RINLY. CHIM. ACTA 56:470-473(1973).
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MEDLINE, 75059220.

MEDLINE, 75059220.

MEDGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
KEUTWANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEUTMANN H.T., NIALL H.D., O'RIORDAN
BIOCHEMISTRY 14:1842-1847(1975).
[8]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOCHEMISTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 91299748
KLAUS W., DIECKMA
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J. CLIN. INVEST. 86:1084-1087(1990).
I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                MARX U.C., AUSTERMANN S., BAYER P., ADERMANN STICHT H., WALTER S., SCHMID F.-X., JAENICKE ROESCH P.;
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MEDLINE; 91009811
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PDB;
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PIR; /
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SEQUENCE
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PROPEP
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MBL; J00301; G190704; -.

MBL; V00597; G37144; -.

MBL; V00597; G37144; -.

MBL; A01536; PTHU.

IR; A01536; PTHU.

IR; A01536; PTHU.

IR; A19339; A19339.
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           Local
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HTH; 15-OCT-97.
LWA: 12-MAR-97.
LWB: 12-MAR-97.
LWC: 12-MAR-97.
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LWC: 16-JUN-97.
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 h 100.0%;
Similarity 100.0%;
5; Conservative
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                                                                                                                        PS00335; PARATHYROID; 1. SIGNAL; DISEASE MUTATION;
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115
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12861
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              Score 35; DB 1;
pred. No. 6.41e+01
                                             PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEI
PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
1; 243E87C7 CRC32;
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       Mismatches
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FORSSMANN
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                                             MEDLINE; 71091588.

MEDLINE; 71091588.

A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., S POTTS J.T. JRAWSON B.F., HOGAN M.L., AURBACH G.D.;

DEFFOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

PROC. TAXIL. ACAD. SCI. U.S.A. 68:63-67(1971).

PROC. TOWN THE ELEVATES CALCIUM LEVEL BY DISSOLVING THE BONE AND PREVENTING THEIR RENAL EXCRETION.

REMBL; V00104; G85; ".

REMBL; J00024; G163641; ".

REMBL; J00024; E18249; ALT_SEQ.

REMBL; V01038; G163647; ".

REMBL; K01038; K1008; K1008
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SEQUENCE FROM N.A.
MEDLINE; 80056617.
KRONENBERG H.M., MCDEVITT B
KRONENBERG H.M., RICH A.;
POTTS J.T. JR., RICH A.;
PROC. NATL. ACAD. SCI. U.S.
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P01268;
21-JUL-1986
21-JUL-1986
01-NOV-1997
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MEDLINE;
WEAVER C.
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EUTHERIA; /
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MEDLINE; 71063634.
BREWER H.B. JR., RON
PROC. NATL. ACAD. SC
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BOS TAURUS
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MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
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MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
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WEAVER C.A., GORDON D.,
MOL. CELL. ENDOCRINOL.
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PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 71076162.
NIALL H.D., KEUTMANN H.T.,
AURBACH G.D., POTTS J.T. J
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MEDLINE; 71076162.
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METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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(REL. 01, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
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NDOCRINOL. 28:411-424(1982).
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                                    PARATHYROID;
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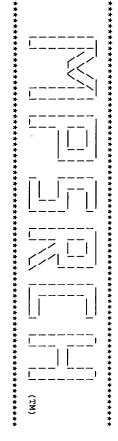
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FT SIGNAL
FT GRADES
FT CHAIN
26 31
FT CONFLICT 106 105
SEQUENCE 115 AA; 12880 MW; 673EASF2 CRC32;

Ouery Match
Best Local Similarity 100.0%; Sco.
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64 NFVAL 68
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Search completed: Thu Jul 30 11:00:22 1998
Job time: 7 secs.
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:00:41 1998; MasPar time 3.58 Seconds 58.840 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-27 (1-5) from US08817547A.pep 35 1 NEVAL 5

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 19.234; Variance 18.297; scale 1.051

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
& & & & & & & & & & & & & & & & & & &	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query
140 2915 342 342 342 3462 3476 4776 533 533 538 538 538 611 1411 1411 1411 1411 1411 1411	Length I
	B
028710 028988 028988 028962 0048962 005074 005074 022162 025119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 0055119 00	Ħ
HYPOTHETICAL 15.7 KD P HYPOTHETICAL 23.8 KD P CONSERVED HYPOTHETICAL ADP-HEPTOSE SYNTHASE. REPB. AUTOTROPHIC GROWTH PRO TO4F8.2. AUTOTROPHIC AT READING EQUINE ARTERITIS VIRUS ARAD. FROM BASES 464774 TO 4 ZK287.2. MULTILDRUG RESISTANCE-L F11_ORF879 PROTEIN. HYPOTHETICAL 151.1 KD POLYPROTEIN 1B (FRAGME POL PROTFIN (CONTA PARATHYROID HORMONE (F HYPOTHETICAL 16.2 KD P	Description
1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02 1.56e+02	Pred. No.

Best Local Similarity 100.0%; Matches 5; Conservative

Pred. No. 1.56e+02; 0; Mismatches 0;

Indels

<u>,,</u>

Gaps

0

HYPOTHETICAL PROTEIN	Q18990 Q18990	2198 3	94.3	ယ္မ	
ASTROTACTIN (NEURO)	Q61137	342 10	ω	္ ယ ယ	<u>-</u> ω
GLYCOPROTEIN B.	096910	322 11	'n	ω ω	42
GLYCOPROTEIN	039989	322 11	'n	<u>კ</u>	41
HOAR.	010611	712 11	w	33	40
NADH DEHYDROGENASE	Q31905	593 6	ω	<b>3</b> 3	39
HIGH AFFINITY SULPHATE	Q43482	560 8	'n	33	38
5-AMINOIMIDAZOLE-4	035567	592 10	'n	33	37
NEURAL SRC INTERACTING	042252	111 12	ω	3 3	36
LIM DOMAIN BINDING	P70060	375 12	'n	<u>ა</u>	35
MATRIX PROTEIN	Q83841	364 11	'n	ω ω	34
MATRIX PROTEIN	Q83838	364 11	w	33	33
MATRIX PROTEIN	Q83832	364 11	'n	ω ω	32
MATRIX PROTEIN	Q83839	364 11	'n	သ	31
MATRIX PROTEIN	Q83836	364 11	'n	ω ω	30
MATRIX PROTEIN	Q83837	364 11	w	33	29
MATRIX PROTEIN	Q83831	364 11	'n	<b>ω</b>	28
MATRIX PROTEIN	Q83833	364 11	w	သ	27
MATRIX PROTEIN	Q83835	364 11	w	33	26
HYPOTHETICAL	P71747	351 9	W	သ	25
YCF4 PROTEIN.	019887	237 6	w	33	24
CYTOCHROME C OXIDASE	Q37451	216 6	'n	33	23
CYCLOPHILIN HOMOLOG	Q94770	196 3	ω	33	22
CKTOCHROME OXIDASE	036547	0	i	i.	21

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Query Match 100.0%; Score 35; DB 9; Length 140;	SEQUENCE 140 AA; 15667 MW; 3AC444AA CRC32;	EMBL; AE000994; G2649000;	SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,	D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,	SPRIGGS T. ARTIACH P. KAINE B.P. SYKES S.M. SADOW P.W.	REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R.,	S.,	QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,	KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D.,	DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L.,	OT AND THE PROPERTY OF THE PRO	SECUTENCE FROM N.A.	SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;	D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,	SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,	., WEIDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D.,	REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R.,	DOUGHERTY B. A. MCKENNEY K. ADAMS M.D. LOFTIUS B. DETTERSON S.	OURCRENBUSH J. LEE N.H. SUTTON G.G. GILL S. KIRKNESS E.F.	D.E. KYRPIDES N.C. FIEISCHMANN R.D.	GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L.	┰	SEQUENCE FROM N.A.	ARCHAEBACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.	ARCHAEOGLOBUS FULGIDUS.		L 15.7 KD PROTEIN.	01-JAN-1998 (TREMBUREL: 05, LAST ANNOTATION UPDATE)	O5, CREA		UT 1 O28710 PRELIMINARY; PRT; 140 AA.

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RESULT
1 P73988;
AC P73988;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL 23.8 KD PROTEIN.
OS SYNECHOCYSTIS SP.
OC EUBACTERIA; CYANOBACTERIA; CHROGCOCCALES; SYNECHOCYSTIS.
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
PM [2]
Search completed: Thu Jul 30 11:01:07 1998 Job time: 26 secs.
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                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-PCC6803;

KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,

MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,

HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,

OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,

YAMADA M., YASUDA M., TABATA S.;

DNA RES. 3:109-136(1996).

EMBL; D90911; G1653142; -.

HYPOTHETICAL PROTEIN.

SEQUENCE 215 AA; 23768 MW; 329FA3F6 CRC32;
                                                                        128 NFVAL 132
|||||
1 NFVAL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 NFVAL 91
|||||
1 NFVAL 5
                                                                                                                                                Score 35; DB 9; Length 215; Pred. No. 1.56e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                      Length 215;
                                                                                                                                                    0;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:04:35 1998; MasPar time 2.73 Seconds 72.991 Million cell upda updates/sec

Tabular output not generated

Title: Description: Perfect Score: (1-13) from US08817547A.pep >US-08-817-547A-28

1 LRKKLQDVHNFVA 13

Scoring table:

Sequence:

PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Listing Match 0% first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.865; Variance 63.388; scale 0.298

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Re

100 100 100 100 100 100 100 100 100 100	No.
<b>,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,</b>	Score
11000.00	Query
60000000000000000000000000000000000000	Length D
7 222 200000007444444444444444444444444444	DB 1
R58173 R58037 R58620 R558230 R588234 R58141 P30015 P30015 P30015 P30015 R21212 R21212 R21212 R21212 R23359 R23359 R23369 R233488 R23488	ID
[Indole-3-carboxylic [L8,A17,Q18,A19]-hPTH [L8,D10,K11,Q18]-hPTH [L8,D10,K11,Q18]-hPTH [Ser14]-hPTH(1-38)-OH [FTH N-terminal.] [Leu21]-hPTH(1-38)-OH Human parathyroid hor Fusion protien comprihuman parathyroid hor Human parathyroid hor Bovine parathyroid hoporcine hoporcine hoporcine hoporcine hoporcine hoporcine hoporcine hopor	Description
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Pred. No.

95 100.0 84 4 R23176 Human parathyroid hor 95 100.0 84 4 R23528 Human parathyroid hor 95 100.0 84 4 R23529 Human parathyroid hor 95 100.0 84 4 R23366 Bovine parathyroid hor 95 100.0 84 4 R23365 Bovine parathyroid hor 95 100.0 84 4 R23276 Bovine parathyroid hor 95 100.0 84 4 R23276 Human parathyroid hor 95 100.0 84 4 R23278 Human parathyroid hor 95 100.0 84 4 R23228 Human parathyroid hor 95 100.0 84 4 R23228 Human parathyroid hor 95 100.0 84 4 R23278 Bovine parathyroid hor 95 100.0 84 4 R23278 Bovine parathyroid hor 95 100.0 84 4 R23278 Bovine parathyroid hor 95 100.0 84 4 R23279 Bovine parathyroid hor 95 100.0 84 4 R23279 Bovine parathyroid hor 95 100.0 84 4 R23279 Bovine parathyroid hor 95 100.0 84 4 R23239 Porcine parathyroid hor 95 100.0 84 4 R23236 Bovine parathyroid hor 95 100.0 84 4 R23231 Human parathyroid hor 9	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
84 4 R23176 Human parathyroid h 84 4 R23529 Human parathyroid h 84 4 R23529 Human parathyroid h 84 4 R23366 Bovine parathyroid 84 4 R23366 Bovine parathyroid 84 4 R23362 Human parathyroid h 84 4 R2326 Bovine parathyroid h 85 W29420 Human parathyroid h 86 4 R23276 Bovine parathyroid h 87 R4995 Sequence of variant 88 4 R23278 Human parathyroid 89 R4995 Sequence of variant 89 R4995 Sequence of variant 80 R4 R23278 Human parathyroid 81 R23428 Human parathyroid 82 R23278 Bovine parathyroid 83 R23279 Bovine parathyroid 84 R23327 Bovine parathyroid 84 R23377 Bovine parathyroid 85 R23439 Porcine parathyroid 86 R23439 Porcine parathyroid 87 R23521 Bovine parathyroid 88 R23379 Bovine parathyroid 89 R23379 Bovine parathyroid 89 R23379 Bovine parathyroid 80 R23379 Bovine parathyroid 81 R23379 Bovine parathyroid 82 R23321 Human parathyroid 83 R23331 Human parathyroid h 84 R23321 Human parathyroid h 85 R23321 Human parathyroid h 86 R233231 Human parathyroid h 87 R23521 Human parathyroid h 88 R23521 Human parathyroid h 89 R23521 Human parathyroid h 89 R23521 Human parathyroid h 80 R23521 Human parathyroid h	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95	95
4 R23176 Human parathyroid h 4 R23528 Human parathyroid h 4 R23529 Human parathyroid h 4 R23366 Bovine parathyroid h 4 R23360 Bovine parathyroid h 6 R23276 Bovine parathyroid h 7 R23276 Human parathyroid h 8 R23276 Sequence of variant h 8 R23278 Bovine parathyroid h 8 R23278 Human parathyroid h 8 R23278 Bovine parathyroid h 8 R23278 Bovine parathyroid h 8 R23329 Bovine parathyroid h 8 R23327 Bovine parathyroid h 8 R23377 Bovine parathyroid h 8 R23379 Bovine parathyroid h 8 R23350 Porcine parathyroid h 8 R23350 Porcine parathyroid h 8 R23379 Bovine parathyroid h 8 R23371 Human parathyroid h 8 R23353 Human parathyroid h 9 R23231 Human parathyroid h 9 R23231 Human parathyroid h		٠		•	•			•					•	•				•	•	•	•		•	•	
R21176  R23528  Human parathyroid h  R23529  Human parathyroid h  R23529  Human parathyroid h  R23365  Bovine parathyroid h  R23276  Human parathyroid h  R21254  Human parathyroid h  R21254  R22376  Bovine parathyroid  R49695  Sequence of variant  R23328  Human parathyroid  R49695  Bovine parathyroid  R23278  Bovine parathyroid  R23278  Bovine parathyroid  R23279  Bovine parathyroid  R23379  Bovine parathyroid  R23370  Bovine parathyroid  R23370  Porcine parathyroid  R23380  Porcine parathyroid  R23370  Bovine parathyroid  R23370  Bovine parathyroid  R23370  Bovine parathyroid  R23371  Bovine parathyroid  R23371  Human parathyroid  R23373  Human parathyroid h	115	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84							
Human parathyroid h Human parathyroid h Human parathyroid h Human parathyroid d Bovine parathyroid d Human parathyroid d Human parathyroid d Human parathyroid d Sequence of variant porcine parathyroid Bovine parathyroid Human parathyroid Human parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Porcine parathyroid Porcine parathyroid Porcine parathyroid Porcine parathyroid Porcine parathyroid Bovine parathyroid Human parathyroid Sequence of preprop	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	9	4	4	35	4	4	4	4	4
Human parathyroid hor Human parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Human parathyroid hor Bovine parathyroid hor Sequence of variant procine parathyroid ho Sequence parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Bovine parathyroid hor porcine parathyroid hor Bovine parathyroid hor Human parathyroid hor Human parathyroid hor Bovine parathyroid hor Human parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Human parathyroid hor Bovine Bovine Parathyroid hor Human hor Hu	P40209	R23231	R23527	R23353	R21214	R23379	R23266	R23389	R23501	R23439	R23277	R23352	R23329	R23278	23	R23428	R49695	R23276	R21254	W29420		336	352	352	R21176
	of	parathyroid	Human parathyroid hor			Bovine parathyroid ho	parathyroid																		

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RESULT THE SOLUTION AND DESCRIPTION AND DESCRI
PR 15-UUL-1992; GB-015009.

PR 18-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026851.

PR 23-DEC-1992; GB-026851.

PR 28-JAN-1993; GB-001691.

PR 28-JAN-1993; GB-001691.

PR 28-JAN-1993; GB-001691.

PR 19-APR-1993; GB-001693.

PR 19-APR-1993; GB-001693.

PR 19-APR-1993; GB-001691.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNCEN VERW GES MBH.

PA (
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20-SEP-1994 (first entry)
[Indole-3-carboxylic acid1]-hPTH(1-36)-NH2.
Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypoparathyroidism.
Synthetic.
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12-JUL-1993;
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/note= "Indole-3-carboxylic acid."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "in amide form"
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RESULT
ID RES
AC RE
AC RE
AC RE
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COMMENT
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ACC R
Search completed: Thu Jul 30 11:04:57 1998 Job time: 22 secs.
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PA (SANO) SANDOZ ERFINDUNGEN VERW GES MBH.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ ERFINDUNGEN VERW GES MBH.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ ERFINDUNGEN VERW GES MBH.

PA (SANO) SANDOZ ERF
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dest Local Similarity 100.0%;
Matches 13; Conservative
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Best Local Similarity 100.0%;
Matches 13; Conservative
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12-JUL-1993; 014384.

15-JUL-1992; GB-015009

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

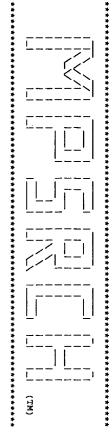
23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-007673.

19-APR-1993; GB-008033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R58052 standard; peptide; 36 AA. R58052; 20-SEP-1994 (first entry) [LB,A17,Q18,A19]-hPTH(1-36)-OH. Human parathyroid hormone; hPTH; variant; calcium; depletion; fixation; resorption; hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB2269176-A.
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                                                                                                                                                                                LRKKLQDVHNFVA
                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                              Score 95; DB 9; Length 36; Pred. No. 6.12e-03; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 95; DB 9; Length 36;
Pred. No. 6.12e-03;
0; Mismatches 0; Indels
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osteopathy; osteoporosis;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:03:49 1998; MasPar time 3.36 Seconds 141.457 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-28 (1-13) from US08817547A.pep 95 1 LRKKLQDVHNFVA 13

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 26.057; Variance 41.730; scale 0.624

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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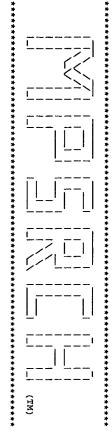
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			•		56.8	•	•	•	•		•			•	•	57.9	57.9	•		٠	
752	421	421	421	421	421	421	421	421	342	189	179	154	911	462	453	305	227	203	119	102	445
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S51866	1SERB	1SETA	1SESB	1SESA	1SETB	S38948	1SRYB	1SRYA	S51402	S59264	I40594	S03242	S28098	A42401	S59436	C64864	A24911	S20584	A34937	S53076	S43492
HPR1 protein – yeast	seryl-tRNA synthetase	serinetRNA ligase (	Seryl-trna synthetase	Seryl-trna synthetase	probable membrane pro	hypothetical protein	_	hypothetical protein	ste6 protein - fissio	macrophage elastase (	hypothetical protein	hypothetical protein	prolactin-like protei	DNA-directed RNA poly	parathyroid hormone p	ne	surface antigen - hep				
3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	3.75e+01	2.63e+01	2.63e+01	2.63e+01		2.63e+01	2.63e+01	2.63e+01	2.63e+01	1.83e+01

Resolu	#authors Marx, U.C. #book in Strukturen Verschiedener Parathormonfragmente in	-references PDB:12WG	Roesch, P.; Marx,	E)	ORGANISM #formal_name synthetic	_NAMES	FIGURE Darathuroid bormone 4 37 mutant	T 2	Db 21 LRKKLODVHNFVA 33	Query Match 100.0%; Score 95; DB 5 Best Local Similarity 100.0%; Pred. No. 1.21e Matches 13; Conservative 0; Mismatches	SUMMARY #length 34 #molecular-weight 4128 #	FEATURE #region helix (right	Š	COMMENT Resolution: not applicable COMMENT Determination: NMR	#book in Strukturen Verschiedener Parathormonfragmente in	TNO	#Submitsion submitted to the biodynavem fiotein #Cross-references PDB:12WE	Roesch, P.; Marx	sapiens	E structure of human	_NAMES HPTH(4-37)	occurred productions
	Parathormonfragmente in Loesung,		Brookhaven Brote'n Data Bank. June 1996		* 017 mmx/ ±0	hormone 4-37, NMR, 10 structures	ant N-TERMINAL SUCCINVLATED -			DB 5; Length 34; 1.21e-06; atches 0; Indels 0; Gaps 0;	t 4128 #checksum 5508	nd alpha)			Parathormonfragmente in Loesung,		ETOCETH Data Bank, Dane 1990	7, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	#common_name man	id normone iragment 4-3/, NMK io	a U.S. statistics	roeddies 4-37) - himan

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Search completed: Thu Jul 30 11:04:18 1998 Job time: 29 secs.
                                                                                                                                                                                                              COMMENT
KEYWORDS
FEATURE
2-9
15-25
SUMMARY
                                                                                                                        Query Match 100.0%; Score 95; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 1.21e-06; Matches 13; Conservative 0; Mismatches 0; Indels
                                                             21 LRKKLQDVHNFVA 33
|||||||||||||
1 LRKKLQDVHNFVA 13
                                                                                                                                                                                                                                                                Determination: NMR
disease mutation; hormone; signal
                                                                                                                                                                                           #region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34  #molecular-weight 4128  #checksum 5508
                                                                                                                      0; Gaps
                                                                                                                        0;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:02:41 1998; MasPar time 2.34 Seconds 139.385 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-28 (1-13) from US08817547A.pep 95 1 LRKKLQDVHNFVA 13

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 27.347; Variance 34.537; scale 0.792

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	ZÉ
3 3 5 5 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	No.
\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$	Score 95
100.0 100.0 97.9 67.4 61.1 61.1 61.7 57.9 57.9 57.9 57.9 57.9 57.9 57.9 56.8	Query Match
	Length 115
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	ID PTHY_CANFA
HORMONE HORMONE HORMONE HORMONE HORMONE HOSPHATE HOSPHATE HOSPHATASE HORMONE H	Description PARATHYROID HORMONE PR
	Pred. No.

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54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	56.8	56.8	56.8
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VP3_AHSV4	MYSP DROME	YO4E MYCTU	URE1_STAXY	GAL7_STRMU	CIT1_SALTY	CIT1_ECOLI	YIE2_HSVB4	FILS_HUMAN	DMD_CHICK	DPOA_TRYBB	MDR1_CAEEL	Y242_MYCPN	YSW1_YEAST	Y397_MYCPN	CILA_HAEIN	HMT1_YEAST	RPOC_SYNPZ	RPOC_PROSC	KINH_NEUCR	HPR1_YEAST	SYS_THETH
OTEIN	5NG F	HYPOTHETICAL 69.2 KD P	UREASE ALPHA SUBUNIT (	GALACTOSE-1-PHOSPHATE	CITRATE-PROTON SYMPORT	CITRATE-PROTON SYMPORT	HYPOTHETICAL PROTEIN I	FILENSIN (LENS FIBER C	DYSTROPHIN.	DNA POLYMERASE ALPHA (	MULTIDRUG RESISTANCE P	HYPOTHETICAL PROTEIN M	SPORE-SPECIFIC PROTEIN	HYPOTHETICAL PROTEIN M	CITRATE LYASE ALPHA CH	HNRNP ARGININE N-METHY	DNA-DIRECTED RNA POLYM	DNA-DIRECTED RNA POLYM	KINESIN HEAVY CHAIN.	HPR1 PROTEIN.	SERYL-TRNA SYNTHETASE
		2.20e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	9.54e+00	9.54e+00	9.54e+00

888	a p p p p p p p p p p p p p p p p p p p	RES AC	Db Qy	Z W O	SHHHA	14222E	RA RC	ROCOS	RES
		RESULT 2 ID PTHY_BOVIN STANDARD; PRT; 115 AA. AC P01268;	55 LRKKLQDVHNFVA 67             1 LRKKLQDVHNFVA 13	Query Match 100.0%; Score 95; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 6.50e-09; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SIGNAL 25 BY SIMILARITY.  SIGNAL 25 BY SIMILARITY.  PROPEP 26 31 BY SIMILARITY.  CHAIN 32 115 PARATHYROID HORMONE.  SEQUENCE 115 AA; 12957 MW; 16EDOEBC CRC32;			CANIS FAMILIARIS (DOG).  CUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  EUTHERIA; CARNIVORA.  [1]	RESULT 115 AA.  RESULT PTY_CANFA STANDARD; PRT; 115 AA.  AC P52212:

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DR FT FT FT FT SQ
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XX MEDLINE; 71091589.

XX MEDLINE; 710924; E18249; ALT_SEQ.

EMBL; 710924; E18249; ALT_SEQ.

EMBL; 710924; E18250; ALT_INIT.

XX MEDLINE; 710928; G163645; -.

XX MEDLINE; 710928; G163645; -.

XX MEDLINE; 710928; G163645; -.
                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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MEDLINE; 71063634.
BREWER H.B. JR., RONI
PROC. NATL. ACAD. SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 82037785.
MEDVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A., POTTS J.T. JR., RICH A.; PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 26-115.

MAEDLINE; 74142666.

MAEDLINE; 75, NIALL H.D., JACOBS J.W., KEUTMANN H.T.,
COHN D.V.;
COH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 80056617.
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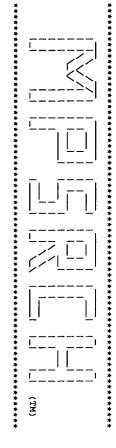
MEDILIE; 71076102.

NIALL H.D., KEUTMANN H.T., SA

AURBACH G.D., POTTS J.T. JR.;

HOPPE-SEYLER'S Z. PHYSIOL. CH
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SEQUENCE
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CHAIN
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    LRKKLQDVHNFVA 13
                             LRKKLQDVHNFVA 67
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115 AA;
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                                                                                                 Pred.
                                                                                                                                     Score 95;
                                                                                                                                                                                        PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
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                                                                                                   Mismatches
                                                                                                                         95; DB 1; I
No. 6.50e-09;
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                                                                                                                                               Length 115;
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                                                                                                      Indels
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                                                                                                   0;
                                                                                                      Gaps
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Search completed: Thu Jul 30 11:02:48 1998 Job time: 7 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. n on: Thu Jul 30 11:03:06 1998; MasPar time 4.15 Seconds 132.066 Million cell updates/sec

Title:

Sequence: Description: Perfect Score: >US-08-817-547A-28 (1-13) from US08817547A.pep 95 1 LRKKLQDVHNFVA 13

Scoring table: РАМ 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mbc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 26.070; Variance 34.227; scale 0.762

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result

20111111111111111111111111111111111111	Result
<b>Რ</b> ᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠᲠ	Score
57.99 57.99 57.99 57.99 57.99	Query Match
105 2475 207 207 320 320 320 320 320 1077 1077 1077 1078 1078 1078 1078 107	Length
10 11 11 11 11 11 11 11 11 11 11 11 11 1	BB
Q063473 Q063473 Q039628 Q05917914 Q94367 Q94367 Q115047 Q115047 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q192974 Q19297	Ħ
PARATHYROLD HORMONE (F POLYPROTEIN PP220. ORF36L. ORF36L. HYPOTHETICAL PROTEIN I MYC PROTEIN (FRAGMENT) F52E10.5 (FRAGMENT) F52E10.5 (FRAGMENT) F52E110.5 (FRAGMENT) F52E110.5 (FRAGMENT) F52E110.5 (FRAGMENT) FOR OR SIMILAR TO SER/THR PRO UBIQUITIN ACTIVATING E PRE S-S ORF. UBIQUITIN ACTIVATING E PRE S-S ORF. UBIQUITIN ACTIVATING E PRE S-S ORF. UBIQUITIN FACTIVATING E PROTHETICAL 50.0 KD P ZINC FINGER PROTEIN (F ZINC FINGER PROTEIN (F ZINC FINGER PROTEIN (F CHLOROQUINE RESISTANCE CHLOROQUINE RESISTANCE CHLOROQUINE RESISTANCE	Description
7.94e-06 4.9e-02 5.27e-0 1.32e+00 2.07e+00 2.07e+00 3.22e+00 3.22e+00 5.01e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00 7.73e+00	Pred. No.

45	44	43	42	41	40	39	3 8	37	36	35	34	<u>ω</u> ω	32	31	30	29	28	27	26	25	24	23	22	21
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RHOPTRY PROTEIN.	MYOSIN.	MYOSIN.	RAD50.	TYPE I RESTRICTION-MOD	PUTATIVE N6-ADEININE S	MYOSIN HEAVY CHAIN 21	OLIGOPEPTIDASE.	Cl3A2.5 PROTEIN.	MYOSIN HEAVY CHAIN (AA	ORF 3.	COSMID F11G11.	T14G8.1 (FRAGMENT).	ZK930.1.	K08E7.9.	SIMILAR TO SACCHAROMYC	C04G6.2 PROTEIN.	SIMILAR TO BACTERIOPHA	DNA-DEPENDENT RNA POLY	SIMILAR TO PROTEIN-TYR	HYPOTHETICAL 104.6 KD	C06G3.9 PROTEIN.	TEKTIN B1.	CHROMOSOME XII COSMID	DNA FOR DTDP-RHAMNOSE
2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.19e+01	1.19e+01	1.19e+01	1.19e+01	1.19e+01	1.196+01

SULT 1 Q63473; Q63473; Q63473; Q63473; Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-NOV-1996 (TREMBLREL. 02, LAST SEQUENCE UPDATE) Q1-NOV-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) Q1-JAN-1998 (TREMBLREL. 01, LAST SEQUENCE GENETICAL SIMILARITY 84, SCORE 83; DB 10; Length 105; Q1-JAN-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-JAN-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-SEM-1997 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-SEM-1997 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 06, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 07, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 08, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 06, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 07, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 08, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 09, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-FEB-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 06, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 07, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TREMBLREL. 08, LAST ANNOTATION UPDATE) Q1-FEB-1997 (TR	IDE ACCOMENTATION ACCOMENTATIO	Db Qy	SO S	א⊢⊄טטטטט
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<b>O</b>	08358  08358;  1-NOV-1996 (TREMBLREL. 01, CREATED)  1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UI  1-EB-1997 (TREMBLREL. 02, LAST ANNOTATION  OLYPROTEIN PP220.  PP2475L.  FRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASTIRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDON  EQUENCE FROM N.A.  EDLINE; 93327788.  IMON-MATEO C., ANDRES G., VINUELA E.;  MBO J. 12:2977-2987(1993).	h 87.4%; Score 83; DB 10; Length 105; Similarity 84.6%; Pred. No. 7.94e-06; 11; Conservative 1; Mismatches 1; Indels 0; KKLQDGHNFVS 57	US NORVEGICUS (RAT).  RYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;  ERIA; RODENTIA.  ENCE FROM N.A.  ENCE FROM N.A.  ENCE FROM D PARATHYROID;  ELIZER H.J., GROSS G., MAYER H.;  GENE TECHNOL. 21:228-229(1984).  TER GENE TECHNOL. 21:228-229(1984).  TER 51  1  ENCE 105 AA; 11746 MW; 6AC3163E CRC32;	1 63473; PRELIMINARY; PR' 63473; 1-NOV-1996 (TREMBLREL. 01, CREA' 1-NOV-1996 (TREMBLREL. 01, LAST 1-AN-1998 (TREMBLREL. 05, LAST ARATHYROID HORMONE (FRAGMENT).

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RN [2]
RN COMPLETE GENOME.
RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGE R.J., CONDRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGE R.J., VINUELA B.;
RL VINOLOGY 208:249-278(1995).
CC -!- FUNCTION: POLYENCTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION CC PROTEINS P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.
DR EMBL; U10466; G780461: -.
KW POLYPROTEIN.
SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3COA CRC32;
QUETY MATCH
Best Local Similarity 75.0%; Pered. No. 4.93e-02;
MATCHES 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 1944 LRKTLQDVISFV 1955
Db 1944 LRKTLQDVISFV 1955
OY 1 LRKKLQDVHNFV 12

Barch completed: Thu Jul 30 11:03:33 1998
Job time: 27 secs.
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(TM)	

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 11:07:12 1998; MasPar time 2.78 Seconds 66.125 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-29 (1-12) from US08817547A.pep 91 1 LRKKLQDVHNFV 12

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45

summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.683; Variance 61.585; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No.	Score	Match	Length	80	Ħ	Description	Pred. No
ָר <u>י</u>	91	100.0	36	ٍ و	R58214	[Ala19]-hPTH(1-36)-NH	1.17e-02
N	91	100.0	36	9	R58213	[D-Ser17]-hPTH(1-36)-	1.17e-02
ω	91	100.0	36	ø	R58286	[D-Leu24]-hPTH(1-36)-	1.17e-02
4	91	100.0	36	ø	R58052	[L8,A17,Q18,A19]-hPTH	1.17e-02
5	91	100.0		26	P30015	Human parathyroid hor	1.17e-02
თ	91	100.0	47	25	W21946	Fusion protien compri	1.17e-02
7	91	100.0		27	W25687	Human parathyroid hor	1.17e-02
œ	91	100.0	84	4	R23545	Bovine parathyroid ho	1.17e-02
ø	91	100.0	84	4	R23354	Bovine parathyroid ho	1.17e-02
10	91	100.0	84	4	R23520		1.17e-02
11	91	100.0	84	4	R23463	Porcine parathyroid h	1.17e-02
12	91	100.0	84	4	R23350	Bovine parathyroid ho	1.17e-02
13	91	100.0	84	4	R23522	Human parathyroid hor	1.17e-02
14	91	100.0	84	4	R21242		1.17e-02
15	91	100.0	84	4	R23273	Bovine parathyroid ho	1.17e-02
16	91	100.0	84	4	R23230	Human parathyroid hor	1.17e-02
17	91	100.0	84	4	R21247	Human parathyroid hor	1.17e-02
18	91	100.0	84	4	R23247	Human parathyroid hor	1.17e-02
19	91	100.0	84	IJ	R29561	Oxidation resistant P	1.17e-02

45	44	43	42	41	40	39	38	37	36	35	3 <b>4</b>	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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P40209	P40252	R21193	R21194	R23417	R21214	R23278	R23279	σ	R21217	R23529	R23329	R21232	R21233	R21239	R23243	R21165	R23439	R21255	o	W29420	R23365	R23344	R23432	R23518	R29562
nce of prepro	Protein including hum	parathyroid	Human parathyroid hor	Porcine parathyroid h	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	e parathyroid	Human parathyroid hor	Human parathyroid hor	Bovine parathyroid ho		Human parathyroid hor			Human parathyroid hor	Porcine parathyroid h	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	Porcine parathyroid h	-	Oxidation resistant [
.17e-	.17e-		.17e-		.17e-	.17e-	7€	.17€	.17e	.17€	.17€	٠	.17€	1	<u>.</u>	<u>.</u>	1	-	.13	.13	1.17e-02	ij	H	17	Ė

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Search completed: Thu Jul 30 11:07:36 1998 Job time : 24 secs.
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PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-001692.
PR 14-APR-1993; GB-001692.
PR 14-APR-1993; GB-001692.
PR 15-MONO SANDOZ PATENT GMBH.
PR (SANO ) SANDOZ GRETON GMBH.
PR (SANO ) SANDOZ
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                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative
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1 LRKKLQDVHNFV 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference 17
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Pred. No. 1.17e-02;
0; Mismatches 0;
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****************** (MT)

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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:06:37 1998; MasPar time 3.31 Seconds 132.368 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-29 (1-12) from US08817547A.pep 91 1 LRKKLQDVHNFV 12

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.786; Variance 40.708; scale 0.633

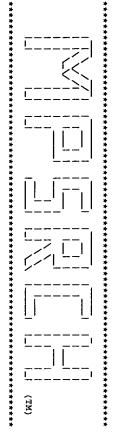
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 4.58e-06 6.77e-00 6.77e+00 9.88e+00 9.88e+00 9.88e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	မ	32	31	30	29	28	27	26	25	24
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S62851	C64043	S45890	S51866	1SERB	1SESB	S38948	1SESA	1SETA	1SRYB	1SRYA	1SETB	S51402	S59264	I40594	S03242	S53076	S28098	A42401	S59436	S43492	C64864
MG397 homolog D02_orf	citrate (pro-3S)-lyas	•	HPR1 protein - yeast	seryl-tRNA synthetase	Seryl-trna synthetase	serinetRNA ligase (	Seryl-trna synthetase	probable membrane pro	hypothetical protein	_	hypothetical protein	probable membrane pro	ste6 protein - fissio	macrophage elastase (	ot 6	é	hypothetical protein				
4.29e+01	4.29e+01	4.29e+01	2.99e+01	2.99e+01					2.99e+01	•		2.99e+01	•	2.99e+01		2.99e+01		2.08e+01	2.08e+01	2.08e+01	2.08e+01

Search completed: Thu Jul 30 11:06:55 1998 Job time : 18 secs. Ą COMMENT
KEYWORDS
FEATURE
2-9
15-25
SUMMARY Βb Query Match
100.0%; Score 91; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.58e-66;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 21 LRKKLQDVHNFV 32 ||||||||||||| 1 LRKKLQDVHNFV 12 Determination: NMR disease mutation; hormone; signal #region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34 #molecular weight 4128 #checksum 5508 0;



MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:06:12 1998; MasPar time 2.30 Seconds 130.665 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-29 (1-12) from US08817547A.pep 91 1 LRKKLQDVHNFV 12

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 27.047; Variance 34.136; scale 0.792

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

77	,	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	ري ري	4	ω	N	<u> </u>	sult
5 5 4 4	54	54	54	54	54	55	55	55	55	55	55	57	57	58	58	60	91	91	91	91	91	Score
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KINH_NEUCR	SYS_THETH	DP3E_BUCAP	YNOO_YEAST	Y17K_SSV1	YM88_YEAST	UBA3_WHEAT	STE6_SCHPO	COGM_MOUSE	HLYE_ECOLI	Y4XD_RHISN	PTHY_CHICK	Y107_METJA	P2C1_YEAST	MYC1_XENLA	GLG2_ARATH	CIT1_KLEPN	PTHY_HUMAN	PTHY_RAT	PTHY_PIG	PTHY_CANEA	PTHY_BOVIN	Ĭ
HPR1 PROTEIN. KINESIN HEAVY CHAIN.	SERYL-TRNA SYNTHETASE	DNA POLYMERASE III, EP	VERY HYPOTHETICAL 21.7		VERY HYPOTHETICAL 11.8	UBIQUITIN-ACTIVATING E	STE6 PROTEIN.	MACROPHAGE METALLOELAS	HEMOLYSIN E (HEMOLYSIN	HYPOTHETICAL 18.0 KD P	PARATHYROID HORMONE PR	HYPOTHETICAL PROTEIN M	PROTEIN PHOSPHATASE 2C	MYC I PROTO-ONCOGENE P	GLUCOSE-1-PHOSPHATE AD	CITRATE-PROTON SYMPORT	PARATHYROID HORMONE PR	Description				
7.94e+00 7.94e+00	7.94e+00	7.94e+00	7.94e+00	7.94e+00	7.94e+00	5.16e+00	5.16e+00	5.16e+00	5.16e+00	5.16e+00	5.16e+00	2.14e+00	2.14e+00	1.36e+00	1.36e+00	5.45e-01	4.71e-08	4.71e-08	4.71e-08	4.71e-08	4.71e-08	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	3 4	<b>ω</b>	32	31	30	29	28	27	26	25	24
51	5	51	51	51	51	51	51	52	52	52	52	52	52	52	52	53	53	53	53	53	53
56.0	56.0	σ.	56.0	ა	σ.	σ	56.0	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	58.2	58.2	58.2	58.2	58.2	58.2
2843	1444	726	360	310	203	134	133	879	636	621	571	491	434	431	269	1339	609	569	500	348	227
н 1	_	Н	μ	μ	μ	μ	μ	Н	μ	j.	μ	μ	μ	<b> </b>	μ.	Н	٢	Н	Ľ	۳	Н
APC_HUMAN	RRPL RDV	ADB2_YEAST	HIS8_LACLA	SYNK_ARATH	RPOC_PROHO	YD89_METJA	YIM5_BPPH1	MYSP_DROME	RPOC_CYAPA	YO4E_MYCTU	URE1_STAXY	GAL7_STRMU	CIT1_SALTY	CIT1_ECOLI	SFAS_CHLEU	DPOA_TRYBB	YSW1_YEAST	Y397_MYCPN	CILA_HAEIN	HMT1_YEAST	PRRA_RAT
ATO	RNA-DIRECTED RNA POLYM	PROBABLE BETA-ADAPTIN	HISTIDINOL-PHOSPHATE A	SYNTAXIN-RELATED PROTE	DNA-DIRECTED RNA POLYM	HYPOTHETICAL PROTEIN M	HYPOTHETICAL IMMUNITY	PARAMYOSIN, LONG FORM.	DNA-DIRECTED RNA POLYM	HYPOTHETICAL 69.2 KD P	UREASE ALPHA SUBUNIT (	GALACTOSE-1-PHOSPHATE	CITRATE-PROTON SYMPORT	CITRATE-PROTON SYMPORT	SF-ASSEMBLIN.	DNA POLYMERASE ALPHA (	SPORE-SPECIFIC PROTEIN	HYPOTHETICAL PROTEIN M	CITRATE LYASE ALPHA CH	HNRNP ARGININE N-METHY	PLACENTAL PROLACTIN-LI
	2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01

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MEDLINE; 71063634.	S Z. PHYSIO	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,	MEDLINE; 71076162.	2	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).		MADULINE; /4142000: HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,			GENE 28:319-329(1984).	62483.	UENCE		DL. 28:411-424	A. GORDON D.F	MEDLINE: 83105964.	UENCE		ACAD SCI U.S.A. 78	MEDLINE; 82037785. WEAVER C.A., GORDON D.F., KEMPER B.:	SEQUENCE FROM N.A.		NATL. ACAD. SCI.	JR., RICH A.;		MEDINE: 80056617.	(L)	EUTHERIA; ARTIODACTYLA.	٠.	BOS TAURUS (BOVINE).		HORMONE PRECUR	(REL. 35, LAST ANNOTATIO	(REL. 01,	21-JUL-1986 (REL. 01, CREATED)	Catherine,	DTHY BOYIN STANDARD. DRT. 115 AA

RESULT
AC PS
AC PS
DT 01
DT 01
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9.0 105 10 Q 7.0 2075 11 Q 7.0 2077 11 Q 7.0 2070 11 Q 32.7 330 12 Q 33.7 591 2 Q 33.7 1291 2 Q 22.6 1070 8 P 12.5 1080 8 P 13.6 10 Q 14.5 11 Q 15.6 10 Q 16.4 1186 10 Q 16.4 2742 3 Q 26.5 3 Q	by analysis of the t SUMMARIE Length DB ID	bl5  fungi 2:sp_human  pho 6:sp_organell  bacteria 10:sp_ro  p_unclassified  5.804; Variance :  nomber of results  n or equal to the	>US-08-817-547A-29 (1-12) from US08817547A.p 91 1 LRKKLQDVHNEV 12 PAM 150 Gap 15 140542 seqs, 42109429 res Minimum Match 08 Listing first 45 summarie	se 3.1A John F. Collins, light (c) 1993-1998 Unive Distribution rights by tein - protein database s Thu Jul 30 11:05:15 199 not generated.	
D HORMONE (F 1.73e-0 N PP220. 3.90e-0 N PP220. 4.26e-0 AL PROTEIN I 1.07e+0 FRAGMENT) 1.69e+0 (0067) FOR OR 1.69e+0 OSER/THR PRO 2.65e+0 ACTIVATING E 2.65e+0 ACTIVATING E 4.14e+0 FR FROTEIN (F 6.42e+0 R PROTEIN (F 6.42e	score distribution.	n ⊬ co ∽i	ep Idues	Biocomputing Research Unit. rsity of Edinburgh, U.K. Oxford Molecular Ltd earch, using Smith-Waterman algorithm 8; MasPar time 3.96 Seconds 127.714 Million cell updates/sec	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
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12	12	ω	N	9	10	10	ω	N	9	9	10	9	ω	10	ø	ω	ω	w	œ	ω	9	و	w	w
P70039	72	Q23669	Q13977		008638		77	~	028565	Ψ	w	P94876	016873	Q63338	Q44535	P91244	Q26216	Q22516	004471	763	P95776	523		a
ADENOMATOUS POLYPOSIS	MYOMESIN.	ZK930.1.	MAJOR YO PARANEOPLASTI	HISC.	MYOSIN.	MYOSIN.	SIMILAR TO PROTEIN-TYR	RAD50.	TYPE I RESTRICTION-MOD	PUTATIVE N6-ADEININE S	MYOSIN HEAVY CHAIN 21	OLIGOPEPTIDASE.	C13A2.5 PROTEIN.	MYOSIN HEAVY CHAIN (AA	ORF 3.	COSMID F11G11.	RHOPTRY PROTEIN (FRAGM	T14G8.1 (FRAGMENT).	SIMILAR TO SACCHAROMYC	C04G6.2 PROTEIN.	DTDP-	HYPOTHETICAL 104.6 KD	C06G3.9 PROTEIN.	TEKTIN B1.
	in	٠	5	.51	2.32e+01	١.,	2.32e+01				2.32e+01		2.32e+01	2.32e+0	:	١.,	1.52e+01	1.52e+0	•	5	:	•	9.91e+00	•

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RESULT 2
10 Q08358
AC Q08358:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DT 01-FEB 1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DC POLYPROTEIN PD220.
GN CP2475L.
GN CP2475L.
OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 93327788.
RA SIMON-MATEO C., ANDRES G., VINUELA E.;
RA EMBO J. 12:2977-2987(1993).
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Best Local Similarity 91.7%;
Matches 11; Conservative
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RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUE-THYROID, AND PARATHYROID;

SCHMELLER H.J., GROSS G., MAYER H.;

ADV. GENE TECHNOL. 21:228-229(1984).

EMBL; M54875; G601933; -.

NON_TER

1 1

SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CT 1
063473 PRELIMINARY; PRT; 105 AA.
063473; O1-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 LRKKLQDGHNFV 56
||||||| ||||
1 LRKKLQDVHNFV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81; DB 10; Le
Pred. No. 1.73e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Parch completed: Thu Jul 30 11:05:54 1998
Job time : 39 secs.
                                                                                                                                                  RN [2]

RP COMPLETE GENOME.

RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA RODRIGUEZ J.F., VINUELA E.;

RL VIROLOGY 208:249-278 (1995).

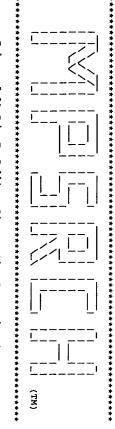
CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION PROTEINS, P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.

CR EMBL; 22777; G394709; -.

DR EMBL; U18466; G780461; -.

SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3COA CRC32;
                                                                                                                                                                                                                  Query Match

72.5%; Score 66; DB 11; Length 2475;
Best Local Similarity 75.0%; Pred. No. 3.90e-02;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps
                                                                  1944 LRKTLQDVISFV 1955
||| ||| :||
1 LRKKLQDVHNFV 12
                                                                                                           ,,
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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:10:20 1998; MasPar time 2.67 Seconds 63.142 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-817-547A-30 (1-11) from US08817547A.pep 84 1 LRKKLQDVHNF 11

Title:

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.206; Variance 59.063; scale 0.308

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	o	ري د	4	ω	N	ш	Result
84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
84	84	84	84	84			36			36	36	36	34				34	34	Length
4	o	4	4	4	27	26	9	9	ø	9	9	9	7	22	22	22	22	26	E E
R23444	R49695	R23253	R23447	R23523	W25687	P30015	R58074	R58285	R58069	R58179	R58184	R58182	R34363	W17959	W17958	W17956	W17957	R62432	Ħ
Porcine parathyroid h	Sequence of variant o	Bovine parathyroid ho	Porcine parathyroid h	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	[L8,Y18]-hPTH(1-36)-O	[Ala23]-hPTH(1-36)-NH	<pre>Isopropyl-[L8,K(Isopr</pre>	[Leu1]-hPTH(1-36)-NH2	[Tyr18]-hPTH(1-36)-NH	[Nva8]-hPTH(1-36)-NH2	Human parathyroid hor	Accelerator peptide b	Description				
	4.45e-02	4.45e-02	4.45e-02	4.45e-02	4.45e-02	4.45e-02	4.45e-02	4.45e-02	4.45e-02	4.45e-02	Pred. No.								

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	04
8	8	8	8	8	8	8	8	8	100.0	8	8	8	00.	8	8	8	٠	8	80.	8	٠	8	80.	80.	8
115	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	*
4	4	4	4	4	G	ر.	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	
P40251	R23323	41	R23381	R23380	R28846	R29562	R23265	R23510	R23311	R21220	R23233	R21207	R21206	R23545	R23354	R23365	R23366	R23464	R23376	R21202	R21203	R21200	R21201	R23483	177171
Protein sequence incl	Bovine parathyroid ho	Porcine parathyroid h	parathyroid	rathyroid	Oxidation resistant [	Oxidation resistant [	Bovine parathyroid ho	Porcine parathyroid h	Bovine parathyroid ho	Human parathyroid hor	parathyroid		parathyroid	Bovine parathyroid ho	parathyroid	Bovine parathyroid ho	Bovine parathyroid ho	Porcine parathyroid h	Bovine parathyroid ho	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Porcine parathyroid h	uniidii paraciiyrotu iior
	.45e-	.45e-	.45e-	.45e-	.45e-	. 45e-	.45e-	.45e-	4.45e-02	.45e-	.45e-	. 45e-	.45e-	. 45e-	5e-	. 45e-	.45e-	.45e-	.45e-	.45e-	. 45	.45e-	Ģ	.45e-	4.400.00

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RESULT
ID WI
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                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative
LT 2
W17957 standard; peptide; 34 AA.
W17957;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Aib3]hPTH(1-34)NH2.
                                                                                                                                                                                                                                                                   Disclosure; Page 3; 7pp; Japanese. The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic amino acids. The accelerator also comprises a cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The accelerator is applied by opening the ginglva, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the epithelium and accelerates fibre adhesion and regenerates cement. Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accelerator for regenerating periodontal tissue - comprises peptide having 3-34 aminoacid residues having connected basic aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-UUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
periodontal tissue; regeneration; periodontitis; periodontal pocket;
down growth; epithelium; fibre adhesion; cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-1993; 045998.
10-FEB-1993; JP-045998.
(SUMZ ) SUNSTAR CHEM IND CO LTD.
WPI; 95-157631/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R62432 standard; peptide; R62432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r06234653-A.
                                                                                                                                                  24 lrkklqdvhnf 34
                                                                                                                              1 LRKKLQDVHNF 11
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                                                                                                                                                                                                Score 84; DB 26;
Pred. No. 4.45e-02;
0; Mismatches (
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                                                                                                                                                                                                    0
                                                                                                                                                                                                                                  Length 34;
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8888888888888
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                                                                                                     밁
                                                                                                                                                                                                   PI Dong 7x;

PI Dong 7x;

PI Dong 7x;

PI New variants of human parathyroid hormone 1-34 peptide - which PT New variants of human parathyroid hormone fracture stimulate bone growth and are used for treatment of osteoporosis and bone fracture claim 11; Page -; 33pp; English.

CC The present sequence is a specific example of a human parathyroid confidence of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 confidence of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 confidence of the aminosisobutyric acid (Aib). In this example the Ser residue at position 3 of the wild-type has been substituted by Aib. The hPTH considered conjunction for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and conjunction with anti-resorptive therapy (bisphosphonates and conjunction with anti-resorptive therapy (bisphosphonates and conjunction because to the known hPTH 1-34 fragment with the modification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim.
                                                                                                                                      Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09702834-A1.
30-JAN-1997.
03-JUL-1996; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_site
                                                                                                                                   y Match 100.0%;
Local Similarity 100.0%;
hes 11; Conservative
                                                                  24 lrkklqdvhnf 34
|||||||||||
1 LRKKLQDVHNF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label≃ Aib
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "In amide form"
                  30 11:10:35 1998
                                                                                                                                      Score 84; DB 22;
Pred. No. 4.45e-02;
0; Mismatches (
                                                                                                                                                                        Length 34;
                                                                                                                                          Indels
                                                                                                                                        0;
                                                                                                                                          Gaps
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:09:33 1998; MasPar time 3.26 Seconds 123.270 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-30 (1-11) from US08817547A.pep

1 LRKKLQDVHNF 11

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.053; Variance 38.928; scale 0.644

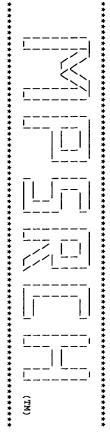
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 3 3 3 4 4 4 4 4 7 7 7 7 8 8 8 7 7 11 11 11 11 11 11 11 11 11 11 11 11	sult No.
888888888886640000000000000000000000000	Score
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parathyroid hormone 4 cyclic parathyroid hormone 6 cyclic parathyroid hormone 6 parathyroid hormone 7 parathyroid hormone 9 parathyroid hormone 9 parathyroid hormone parathyroid	Description
4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 1.77e+00 5.81e+00 1.25e+01 1.25e+01 1.25e+01 1.25e+01 1.25e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	ω S	34	33	32	31	30	29	28	27	26	25	24
51	51	52	52	52	52	53	53	53	53	53	54	54	54	54	54	54	54	54	54	54	54
60.7	60.7	61.9		61.9	61.9	•	63.1	63.1	63.1	63.1	64.3		64.3	64.3	64.3	64.3		64.3	64.3	64.3	64.3
431	360	957	879	878	571	569	500	348	227	102	752	421	421	421	421	421	421	421	421	342	189
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ZTEC3	B45734	C69463	S22028	S20486	S38485	S62851	C64043	S45890	A24911	S53076	S51866	1SERB	1SESB	1SESA	1SETB	1 SETA	1SRYB	1SRYA	S38948	S51402	S59264
citrate utilization d	HisC - Lactococcus la	type I restriction-mo	paramyosin, standard	paramyosin - fruit fl		MG397 homolog D02_orf	citrate (pro-3S)-lyas	ODP1 protein - yeast	prolactin-like protei	probable membrane pro	HPR1 protein - yeast	seryl-tRNA synthetase	serinetRNA ligase (	probable membrane pro	hypothetical protein						
5.53e+01	5.53e+01	3.84e+01	3.84e+01	٠	3.84e+01		2.66e+01	2.66e+01	2.66e+01	2.66e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01

PDB_TITLE  Structure of NNR, 10 st ORGANISM #formal_name REFERENCE A67742 P.;  #authors Roesch, P.;  #submission submitted to to #cross references PDB:12WF REFERENCE Marx, U.C.  #book in Strukture	QY 1 LRKKLQDVHNF RESULT 2 1ZWF ENTRY para TITLE para SY ALTERNATE NAMES n-ac	Query Match 100.0%; Best Local Similarity 100.0%; Matches 11; Conservative	15-25 SUMMARY	rs	REFERENCE A6//43 #authors Roesch, P.; #submission submitted to #cross references PDB:12WG REFERENCE THOO3319	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM
structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures #formal_name synthetic A67742 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 noes pdB:IZWF TN003318 Marx, U.C. Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung,	)VHNF 11  12WF	tch 100.0%; Score 84; DB 5; Length 34; al Similarity 100.0%; Pred. No. 4.83e-05; 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; IRKKIODVHNE 31	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	Marx, U.C.  In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR disease mutation; hormone; signal	Ab//43 Roesoh, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nees PDB:1ZWG TN003319	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic n-succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic



(Psrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:07:53 1998; MasPar time 2.18 Seconds 126.596 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-30 (1-11) from US08817547A.pep 84 1 LRKKLQDVHNF 11

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 26.284; Variance 32.770; scale 0.802

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

sult	Score	Query Match	Length	BB	Ħ	Description	Pred. No.
_ :	84	100.0	115	٠.,	PTHY_BOVIN	PARATHYROID HORMONE PR	9.02e-07
N	84	100.0	115	<b>ب</b>	1 1	_	9.02e-07
w	84	100.0	115	ا	PTHY_PIG		9.02e-07
4	84	100.0	115	Н	PTHY_RAT	PARATHYROID HORMONE PR	
տ	84		115	۲	PTHY_HUMAN	PARATHYROID HORMONE PR	9.02e-07
σ	60	•	444	1	CIT1_KLEPN	CITRATE-PROTON SYMPORT	2.85e-01
7	57	•	184	۳	GLG2_ARATH	GLUCOSE-1-PHOSPHATE AD	1.17e+00
<b>&amp;</b>	55	•	119	_	PTHY_CHICK	PARATHYROID HORMONE PR	2.91e+00
9	55	•	162	_	Y4XD_RHISN	HYPOTHETICAL 18.0 KD P	2.91e+00
10	55	•	305	1	HLYE_ECOLI	HEMOLYSIN E (HEMOLYSIN	2.91e+00
11	ភភ	•	462	ب	COGM_MOUSE	MACROPHAGE METALLOELAS	
12	54	•	189	1	YNOO_YEAST	VERY HYPOTHETICAL 21.7	4.56e+00
13	54	64.3	233	_	DP3E_BUCAP	DNA POLYMERASE III, EP	4.56e+00
14	54	•	421	μ.	SYS_THETH	SERYL-TRNA SYNTHETASE	4.56e+00
<u>1</u> 5	54	•	752	Н	HPR1_YEAST	HPR1 PROTEIN.	4.56e+00
16	53	63.1	102	۲	YM88_YEAST	VERY HYPOTHETICAL 11.8	7.08e+00
17	53	•	227	ب	PRRA_RAT	PLACENTAL PROLACTIN-LI	7.08e+00
18	53	63.1	348	٢	HMT1_YEAST	HNRNP ARGININE N-METHY	7.08e+00
19	53	•	500	μ	CILA_HAEIN	CITRATE LYASE ALPHA CH	7.08e+00
20	53	•	569	۳	Y397_MYCPN	HYPOTHETICAL PROTEIN M	7.08e+00
21	52	•	571	Н	URE1_STAXY	UREASE ALPHA SUBUNIT (	1.09e+01
22	52	61.9	621	Н	YO4E_MYCTU	HYPOTHETICAL 69.2 KD P	1.09e+01
23	52	•	879		MYSP_DROME	PARAMYOSIN, LONG FORM.	1.09e+01

4 4 5 4	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24
50 49	50	50	50	50	50	50	50	50	50	50	51	51	51	51	51	51	51	51	51	51
59.5 58.3	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7
4725 455	1314	1257	610	610	609	586	525	510	437	281	2843	1444	434	431	419	360	317	310	133	111
μμ	بر	<b>j3</b>	ᆫ	_	<u>, , , , , , , , , , , , , , , , , , , </u>	ᆫ	Ц	Ц	_	_	Ц	L	<b></b> 4	Н	Н	ب	ب	ь	ட	1
YHCL_ECOLI	SS22_YEAST	RBB1_HUMAN	LKHA HUMAN	LKHALMOUSE	LKHA_RAT	YM61_CAEEL	Y107_METJA	CILA_ECOLI	FOLC_HAEIN	P2C1_YEAST	APC_HUMAN	RRPL_RDV	CIT1_SALTY	CIT1_ECOLI	MYC1_XENLA	HIS8_LACLA	MSHR_BOVIN	SYNK_ARATH	YIMS_BPPH1	ARPP_BOVIN
HYPOTHETICAL 48.8 KD P	SERINE/THREONINE PROTE	H WWC	A-4	LEUKOTRIENE A-4 HYDROL	LEUKOTRIENE A-4 HYDROL	HYPOTHETICAL 65.8 KD P	HYPOTHETICAL PROTEIN M	CITRATE LYASE ALPHA CH	FOLYLPOLYGLUTAMATE SYN	PROTEIN PHOSPHATASE 2C	ADENOMATOUS POLYPOSIS	RNA-DIRECTED RNA POLYM	CITRATE-PROTON SYMPORT	CITRATE-PROTON SYMPORT	MYC I PROTO-ONCOGENE P	HISTIDINOL-PHOSPHATE A	MELANOCYTE STIMULATING	SYNTAXIN-RELATED PROTE	HYPOTHETICAL IMMUNITY	CAMP-REGULATED PHOSPHO
2.56e+01 3.87e+01				2.56e+01	2.56e+01	2.56e+01	2.56e+01	2.56e+01	2.56e+01	2.56e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01

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SO SO
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                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative
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Best Local s
Matches 1
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A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

L PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

C -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SCHMEL; VO0106; 685; -.

DONE AND PREVENTING THEIR RENAL EXCRETION.

REMBL; V00024; G163641; -.

REMBL; J00024; G163643; -.

REMBL; J00024; E18259; ALT_SEQ.

DR EMBL; J00024; E18269; ALT_SEQ.

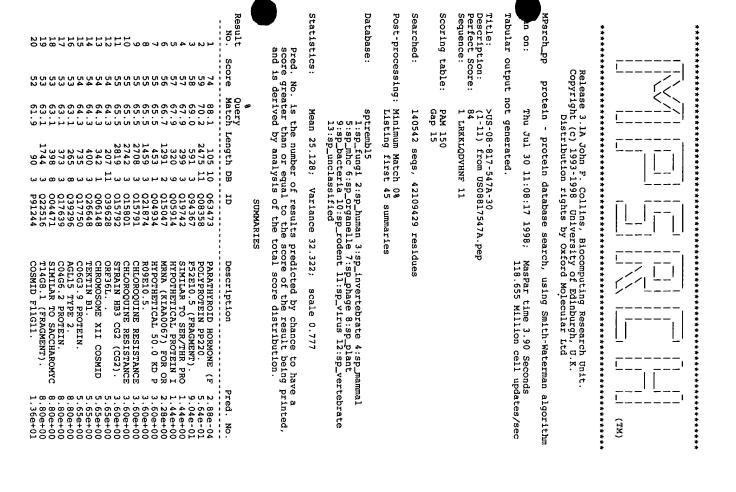
DR EMBL; V00028; G163647; -.

DR EMBL; M01938; G163645; -.

DR EMBL; M15082; G163645; -.
                                                                                                                                                                                 PROSITE; PS00335; PARATHYROID; 1.
PROSITE; PS00335; PARATHYROID; 1.
PROSIDED: 1 25 BY SIM
PROPED: 26 31 BY SIM
PROPED: 32 115 PARATH
SEQUENCE: 115 AA; 12957 MW; 16ED
                                                                                                                                                                                                                                                                                                                                  TISSUS-PARATHYROID;
MEDLINE; 9539696.
ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
DEWILLE J.W., CAPEN C.C.;
GENE 160:241-243(1995).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
EMB; U15662; G558916; ---
EMB; U15662; G558916; ---
EMB; U15662; G558916; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTHY_CANFA STANDARD; PRT; 115 AA.
P52212;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
PROPEP
CHAIN
CONFLICT
SEQUENCE
                               55 LRKKLQDVHNF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01534; PTBO.
PIR; A24949; A24949.
PROSITE; PS00335; PARATHYROID; 1.
1 LRKKLQDVHNF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHESIS
MEDLINE; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BREWER H.B. PROC. NATL. [8]
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Local Similarity 100.0%;
nes 11; Conservative
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1
26
32
106
115 AA;
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. SCI. U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
31
115 PARATHYROID HORMONE.
106 V -> G (IN REF. 4).
12980 MW; 673EASF2 CRC32;
                                                                                 Score 84; DB 1; Ler
Pred. No. 9.02e-07;
0; Mismatches 0;
                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
W; 16ED0EBC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84; DB 1; Length 115;
Pred. No. 9.02e-07;
0; Mismatches 0; Indels
                                                                                                                                 Length 115;
                                                                                    Indels
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                                                                               0;
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                                                                         Gaps
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Ş В

Search completed: Thu Jul 30 11:08:00 1998 Job time : 7 secs.



	45	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	ω ω	32	<u>3</u> 1	30	29	28	27	26	25	24	23	22	21	
	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	52	52	52	52	52	52	
	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	61.9	61.9	61.9	61.9	61.9	61.9	
	2845	2844	2842	2829	2743	1630	1444	1200	733	385	360	330	317	317	257	242	242	231	110	1312	957	929	602	485	160	
	10	N	10	12	N	2	1	9	ω	ω	٥	12	4	4	œ	æ	œ	و	4	N	9	ø	9	ω	9	
AT TOWNSHIPS	Q61315	Q15163	P70478	P70039	Q15162	Q90724	Q98631	P73340	Q24250	017076	034130	Q91794	P79328	019037	Q40700	P93468	Q40970	Q55290	P79322	Q92878	028565	032491	P94876	016873	Q44535	
	ADENOMATOSIS POLYPOSIS	POLYPOSIS LOCUS-ENCODE	APC PROTEIN.	ADENOMATOUS POLYPOSIS	POLYPOSIS LOCUS-ENCODE	MYOMESIN.	RNA-DEPENDENT RNA POLY	CHROMOSOME SEGREGATION	TARTAN PROTEIN PRECURS	C38C3.3 PROTEIN.	HISC.	MYC PROTEIN (FRAGMENT)	MELANOCYTE STIMULATING	MC1-R PROTEIN.	BOX PROTEIN.	MADS-BOX FAMILY TRANSC	PUTATIVE MADS-BOX FAMI	ORF10.	CAMP-REGULATED PHOSPHO	RAD50.	TYPE I RESTRICTION-MOD	PUTATIVE N6-ADEININE S		Cl3A2.5 PROTEIN.	ORF 3.	
	2.10e+01	•	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	1.36e+01	1.36e+01	1.36e+01	1.36e+01	1.36e+01	1.36e+01	

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         RESULT

RESULT

QU

AC QU

DT 01

DT 01

DT 02

CT

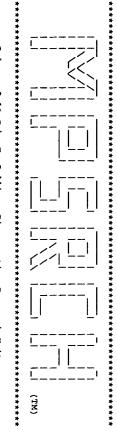
GN CT

RN CT

RN [1]

RN [1]
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Best Local
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                                                                                                                                                                                                                                ULT 2
Q08358
Q08358;
01-NOV-1996 (TREMBL)
01-FEB-1997 (TREMBL)
POLYPROTEIN PP220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q63473;
Q63473;
Q1-NOV-1996
Q1-NOV-1996
Q1-JAN-1998
                                                                                                                                                                               CP2475L.
AFRICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MON_TER
SEQUENCE FROM N.A.
MEDLINE; 93327788.
SIMON-MATEO C., ANDRES G.,
EMBO J. 12:2977-2987(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-THYROID, AND PARATHYROID;
SCHWELZER H.J., GROSS G., MAYER
ADV. GENE TECHNOL. 21:228-229(19
EMBL, M54875; G601933; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UF
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION
PARATHYROID HORMONE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOR
EUTHERIA; RODENTIA.
                                                                                                                                                    VIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 LRKKLQDGHNF 55
|||||| |||
1 LRKKLQDVHNF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 88.1%;
Local Similarity 90.9%;
                                                                                                                                                 SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).
; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                 5 (TREMBLREL.
6 (TREMBLREL.
7 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 AA; 11746 MW;
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                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSS G., MAYER H.;
21:228-229(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                 01, CREATED)
01, LAST SEQUENCE UPDATE)
02, LAST ANNOTATION UPDATE)
                                    VINUELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74; DB 10;
Pred. No. 2.88e-04;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6AC3163E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                       2475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
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RN [2]
RP COMPLETE GENOME.
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUES C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUES C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUES C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ L., NOGAL M.J., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ L., YUSTE L., ENRIQUEZ C.,
RA YANGER R.J., RODRIGUEZ L., YUSTE L., ENRIQUEZ C.,
RA RODRIGUEZ R.J., RODRIGUEZ L., YUSTE L., ENRIQUEZ C.,
RA RODRIGUEZ R.J., RODRIGUEZ L., YUSTE L., ENRIQUEZ C.,
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RA RODRIGUEZ L., RODRIGUEZ L., YUSTE L., YUSTE L., ENRIQUEZ C.,
RA RODRIGUEZ L., YUSTE L., YUSTE
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MPsrch_pp m on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:12:42 1998; MasPar time 2.67 Seconds 57.535 Million cell updates/sec

Tabular output not generated.

Description: Title: >US-08-817-547A-31 (1-10) from US08817547A.pep 73

Sequence: Perfect Score: 1 LRKKLQDVHN 10

Scoring table:

PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match Listing first 45 summaries

Database: a-geneseq31-2

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 17.167; Variance 59.785; scale 0.287

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No. Score Match Length	73	2 73 100.0	73	73	5 73 100.0	73	73	73	73		73		73		73	č	73	73 73	16 73 100.0 17 73 100.0 18 73 100.0
	33	<b>3</b> 4	34	34	34	34	34	34	34	34	34	34	35	35	35	36	36	36	
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ID	R88841	R62432	R45508	R45528	R69037	R34353	R34352	R34345	R41582	W20002	W20003	W17962	R74442	R74413	R74527	R58243	R58057	85803K	100000
Description	Human parathyroid hor	erator peptid	Parathyroid hormone/p	Parathyroid hormone/p	PTH analogue with amp	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	[Arg15,16,17]hPTH (1-	Cyclised rat parathyr	Cyclised [Nle 8,18, T	Human PTH analogue [C	Parathyroid hormone p	Parathyroid hormone p	Human parathyroid hor	Propargyl-[Al]-hPTH(1	[L8,D10,A16,Q18]-hPTH	N-alpha-methyl[Ala1]	
Pred. No.	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	

73 100.0 38 9 R58091 [Ile]-j-hPTH(1-38)-OH 73 100.0 38 9 R580929 [Thr]-hPTH(1-38)-OH 73 100.0 38 9 R58029 [Thr]-hPTH(1-38)-OH 73 100.0 38 9 R58028 [Thr]-hPTH(1-38)-OH 73 100.0 38 9 R58028 [Lys19]-hPTH(1-38)-OH 73 100.0 84 27 W25687 Human parathyroid hor 73 100.0 84 4 R23242 Human parathyroid hor 73 100.0 84 4 R23521 Bovine parathyroid hor 73 100.0 84 4 R23242 Human parathyroid hor 73 100.0 84 4 R23242 Human parathyroid hor 73 100.0 84 4 R23243 Bovine parathyroid hor 73 100.0 84 4 R23346 Bovine parathyroid hor 73 100.0 84 4 R23336 Bovine parathyroid hor 73 100.0 84 4 R23229 Human parathyroid hor 73 100.0 84 4 R23239 Human parathyroid hor 73 100.0 84 4 R23236 Human parathyroid hor 73 100.0 84 4 R23251 Bovine parathyroid hor 73 100.0 84 4 R23256 Human parathyroid hor 73 100.0 84 4 R23256 Human parathyroid hor 73 100.0 84 6 R30857 Cys35 hPTH mutein 73 100.0 84 4 R21241 Human parathyroid hor 73 100.0 84 4 R21241 Human parathyroid hor 73 100.0 84 4 R21240 Human parathyroid hor 73 100.0 84 4 R21241 Human parathyroid hor 73 100.0 84 4 R21240 Porcine parathyroid hor 73 100.0 84 4 R21240 Porcine parathyroid hor 73 100.0 84 4 R23474 Porcine parathyroid hor	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	60
38 9 R58061 [Ile15]-hPTH(1-38)-O 38 9 R58091 [Cys13]-hPTH(1-38)-O 38 9 R58092 [Thr1]-hPTH(1-38)-O 38 9 R58028 [Thr1]-hPTH(1-38)-O 38 9 R58124 [Lys19]-hPTH(1-38)-O 38 4 R23521 [Bovine parathyroid ho 38 4 R2345] [Human parathyroid ho 39 4 R23242 [Human parathyroid ho 30 84 4 R23243 [Human parathyroid ho 30 84 4 R23241 [Human parathyroid ho 30 84 4 R23217 [Human parathyroid ho 30 84 4 R23251 [Human parathyroid ho 31 84 4 R23251 [Human parathyroid ho 32 84 R23251 [Human parathyroid ho 38 4 R23251 [Human parathyroid ho 39 84 R23368 [Bovine parathyroid ho 30 84 R23368 [Bovine parathyroid ho 30 84 R23261 [Human parathyroid ho 30 84 R23261 [Human parathyroid ho 31 R23474 [Human parathyroid ho 32 R23474 [Human parathyroid ho 33 R23474 [Human parathyroid ho 34 R232474 [Human parathyroid ho 35 R23474 [Human parathyroid ho 36 R30856 [Cys35 hPTH muttein ho 36 R30856 [Cys35 hPTH muttein ho 37 R23474 [Human parathyroid ho 38 R23475 [PTH muttein ho	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	;
8 9 R58001 [Ilels]-hprH(1-38)-0 8 9 R58091 [Cysl3]-hprH(1-38)-0 8 9 R58092 [Thr]-hprH(1-38)-0 8 9 R58028 [Thr]-hprH(1-38)-0 8 9 R58114 [Lysl9]-hprH(1-38)-0 9 R58114 [Lysl9]-hprH(1-38)-0 4 26 P30015 Human parathyroid ho 4 27 W25687 Human parathyroid ho 4 R23243 Porcine parathyroid ho 4 R23322 Human parathyroid ho 4 R23324 Human parathyroid ho 4 R23324 Human parathyroid ho 4 R23326 Bovine parathyroid ho 4 R23326 Human parathyroid ho 4 R23329 Human parathyroid ho 4 R21198 Human parathyroid ho 4 R21198 Human parathyroid ho 4 R23356 Human parathyroid ho 5 R30856 Leul8 hprH mutein. 6 R30856 Cys35 hprH mutein. 6 R30856 Cys35 hprH mutein. 6 R30856 Leul8 hprH mutein. 6 R30856 Human parathyroid ho 6 R31240 Human parathyroid ho 6 R31240 Human parathyroid ho 6 R30856 Cys35 hprH mutein. 6 R30856 Cys35 hprH mutein. 6 R30856 Parathyroid ho 7 R23474 Parathyroid ho		٠			٠		٠	٠		•			•			•			•	•		٠	•	•	٠	٠
R58061 [ILE] - hPHH(1-38) - OR580691 [Cys13] - hPHH(1-38) - OR58028 [Thr1] - hPHH(1-38) - OR58028 [Thr1] - hPHH(1-38) - OR58028 [Lys19] - hPHH(1-38) - OR58028 [Lys19] - hPHH(1-38) - OR5687 Human parathyroid ho R21244 Human parathyroid ho R23453 POrcine parathyroid ho R23453 Human parathyroid ho Bovine parathyroid ho R23346 Bovine parathyroid ho R23346 Human parathyroid ho R23359 Human parathyroid ho R23119 Human parathyroid ho R23119 Human parathyroid ho R23126 Human parathyroid ho R23124 Porcine parathyroid ho R231240 Porcine parathyroid ho R231475 Porcine Parathyroid ho Parathyroi	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	4	4	œ	œ	8	œ	•
[TISTS] -hPTH(1-38) O [Cys13] -hPTH(1-38) O [Thr1] -hPTH(1-38) O [Thr1] -hPTH(1-38) O Human parathyroid ho Human parathyroid ho Human parathyroid ho Bovine parathyroid ho Human parathyroid ho Human parathyroid ho Bovine parathyroid ho Bovine parathyroid ho Human parathyroid ho Human parathyroid ho Human parathyroid ho Human parathyroid ho Bovine parathyroid ho Human parathyroid ho Human parathyroid ho Bovine parathyroid ho Bovine parathyroid ho Bovine parathyroid ho Bovine parathyroid ho Bovine parathyroid ho Bovine parathyroid ho Porcine parathyroid ho Porcine parathyroid ho	4	4	4	4	σ	σ	4	4	4	4	4	4	4	4	4	4	4	4	4	27	26	9	ø	9	ဖ	,
5] hpHH(1-38) O 1] hpHH(1-38) O 1] hpHH(1-38) O 9] hpH(1-38) O 9] hpH(1-38) O parathyroid ho parathyroid ho	347	347	12	R21241	R30856	R30857	R23368	R21256	R23251	R21198	R21217	R23529	R23336	R23346	R23241	R23242	R23453	R23521	R21244	W25687	-ب	812	802	608	908	0
	parathyroid	parathyroid	parathyroid ho	parathyroid ho	Cys35 hPTH mutein.	Leu18 hPTH mutein.	e parathyroid	19]-hPTH(1-38)	1]-hPTH(1-38)-	13]-hPTH(1-38)-C	15]-hPTH(1-38)-	18 111 111 1 10 / 0														

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Best Local Similarity 100.0%;
Matches 10; Conservative
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20-JUN-1994; CA-126299.
(WILL/) WILLICK G E.
Neugebbuer W. Sung WL,
Willick GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human parathyroid hormone analogues - which have increased adenylyl cyclase activating activity, used for treating osteoporosi Claim 2; Page -; 21pp; English.

R88829-R88841 are human parathyroid hormone (hPTH) analogues. The analogues increase G-protein coupled adenylyl cyclase (cAMPase) activity and reduce protein kinase C (PKC) activity. The analogues can reverse the loss of bone and increase bone mass and density without undesirable effects. They are useful for the treatment of osteoporosis and other bone related disorders and disorders involving bone cell calcium regulation.
л 2
R62432 standard; peptide; 34 AA.
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21-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         increased adenylyl cyclase activity; synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human parathyroid hormone analogue, [Leu27]-hPTH(1-33)-NH2. Parathyroid hormone; PTH; analogue; osteoporosis; bone cell; calcium regulation; reduced PKC activity; protein kinase C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R88841;
07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R88841 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone cell
33 AA;
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33
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                                                                                                                                                                                                                                                                                                          Score 73; DB 18; Le
Pred. No. 8.53e-01;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                 Length 33;
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AR R62432;
DT 31-UII-1995 (first entry)
DE Accelerator peptide basic region peptide, P-8.

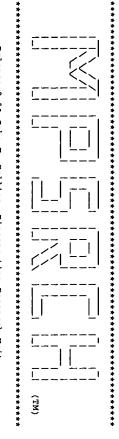
RW Accelerator; basic amino acid; cell growth factor; growth; gingiva; periodontal tissue; regeneration; periodontitis; periodontal pocket; Synthetic.

RW down growth; epithelium; fibre adhesion; cement.

PN U6234653-A.

PD 23-AUG-1994.

PN 10-EB-1993; 045998.
PR 10-EB-1993; JP-045998.
PR 1
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

in on: Thu Jul 30 11:12:07 1998; MasPar time 3.23 Seconds 113.195 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-31 (1-10) from US08817547A.pep 73-

1 LRKKLQDVHN 10

Scoring table:

PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 23.845; Variance 36.931; scale 0.646

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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\$5\$\$\$\$5\$\$\$5\$\$3333333333333333333333333	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	% Query Match
34 34 34 35 35 35 35 35 35 35 35 35 35 36 37 37 37 42 37 42 31 42 31 42 31 42 31	Length
<b></b>	BB
1ZWG 1ZWE 1HTH 1ZWE 1ZWD 1ZWD 1ZWD 1ZWD 1ZWD 1ZWC PTPG PTPG PTPG PTPG PTPG PTPG PTPG PTP	ID
004000000000000000000000000000000000000	Description
99999940000000000000000000000000000000	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
49	49	49	49	50	50	50	50	50	50	50	50	51	51	51	51	52	52	52	53	53	54
67.1	67.1	67.1	67.1	68.5	68.5	68.5	68.5	68.5	68.5	68.5	68.5	69.9	69.9	69.9	69.9	71.2	71.2	71.2	72.6		74.0
899	630	444	215	4725	1972	1938	621	586	437	412	360	1200	571	317	257	2475	879	878	569	348	421
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S51341	C64302	S09681	S35640	A44357	JC5420	JC5421	S10450	S44850	C64113	S07537	B45734	S77524	S38485	S45708	S53306	S35307	S22028	S20486	S62851	S45890	1SERB
probable membrane pro	hypothetical protein	citrate transport pro	hypothetical protein	dynein heavy chain, c	smooth muscle myosin	smooth muscle myosin	myosin heavy chain -	K12H4.1 protein - Cae	tetrahydrofolylpolygl	myosin heavy chain, c	HisC - Lactococcus la	chromosome segregatio	urease (EC 3.5.1.5) 6	MSH receptor - bovine	floral homeotic prote	polyprotein pp220 pre	paramyosin, standard	paramyosin – fruit fl	MG397 homolog D02_orf	ODP1 protein - yeast	seryl-tRNA synthetase
6.04e+01	6.04e+01	6.04e+01	6.04e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	2.87e+01	2.87e+01	2.87e+01	2.87e+01	1.97e+01	1.97e+01	1.97e+01	1.34e+01	1.34e+01	9.09e+00

RESULT 2 12WF ENTRY parathyroid TITLE synthetic ALTERNATE_NAMES n-acetyl-hpt PDB_TITLE structure of PDB_TITLE NMR, 10 st ORGANISM #formal_name REFERENCE #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07742 #07	Query Match Best Local Similar Matches 10; Co Db 21 LRKKLQDVHN            Qy 1 LRKKLQDVHN	RESULT 1 1ZWG #1 ENTRY parathyroid   TITLE synthetic   ALTERNATE_NAMES n-succinyl-hyper   PDB_TITLE   PDB_TITLE   PDB_TITLE   PDB_TITLE   PDB_TITLE   PDB_TITLE   PDB_TITLE   PDCCTMAL   PDCCTMAL   POCK   PO
12WF #type complete parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures #formal_name synthetic A67742 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces pDB:1ZWF TN003318 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, in Strukturen Verschiedener Parathormonfragmente in Loesung,	Query Match 100.0%; Score 73; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 2.82e-03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 21 LRKKLQDVHN 30           1 LRKKLQDVHN 10	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic A67743

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COMMENT RESOLUTION: not applicable
RETWORDS

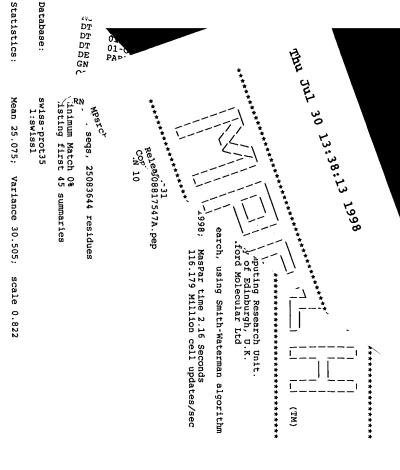
FEATURE
1-6
14-27

SUMMARY

Query Match
Best Local Similarity 100.0%; Score 73; DB 5; Length 34;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LRKKLODVHN 30
Quy 1 LRKKLODVHN 10
Search completed: Thu Jul 30 11:12:24 1998

Search completed: Thu Jul 30 11:12:24 1998
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARI

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Y019_METJA Y17K_SSV1 YXDJ_BACSU	VS10_ROTBS CIT1_KLEPN	FOLC_HAEIN	MSHR_BOVIN URE1_STAXY HIS8_LACLA	MYSP_DROME SYNK_ARATH	Y397_MYCPN	SYS_THETH HMT1_YEAST	PTHY_HUMAN	PTHY_RAT	PTHY_CANFA	PTHY BOVIN	ID
HYPOTHETICAL PROTEIN M HYPOTHETICAL 17.8 KD P HYPOTHETICAL 26.6 KD S	MINOR OUTER CAPSID PRO CITRATE-PROTON SYMPORT	FOLYLPOLYGLUTAMATE SYN HYPOTHETICAL 65.8 KD P DYNEIN HEAVY CHAIN. CY	MELANOCYTE STIMULATING UREASE ALPHA SUBUNIT ( HISTIDINOL-PHOSPHATE A	PARAMYOSIN, LONG FORM. SYNTAXIN-RELATED PROTE	HYPOTHETICAL PROTEIN M HYPOTHETICAL 69.2 KD P	SERYL-TRNA SYNTHETASE HNRNP ARGININE N-METHY	PARATHYROID HORMONE PR	HORMONE	HORMONE	PARATHYROID HORMONE PR	Description
1.66e+01 2.56e+01 2.56e+01	1.66e+01	1.07e+01 1.07e+01 1.07e+01	6.80e+00 6.80e+00 1.07e+01		2.72e+00 4.31e+00	1.70e+00 2.72e+00	8.74e-05 1.06e+00	8.74e-05	.746	8.74e-05	Pred. No.

44 5	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24
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637 1679	590	475	457	380	326	297	1225	1036	911	752	189	112	100	2663	1126	926	920	857	669	419
11	۲	ᆫ	<u>,                                    </u>	Н	ㅂ	μ	μ	ш	ш	μ	μ	μ	-ب	Ь	μ.	<u>,</u>	_	Н	Н	Ц
PTMA_ECOLI	YM63_YEAST	2131_HUMAN	EMB8_PICGL	CAPM_STAAU	YIE1_YEAST	YUBO_CAEEL	SMC1_YEAST	YAN2_SCHPO	STE6_SCHPO	HPR1_YEAST	YNOO_YEAST	YI91_SHIDY	YI91_ECOLI	CENE_HUMAN	RPOB_SULAC	POOL_HAEIN	YML1_YEAST	MEDB_GIALA	YMS2_YEAST	PEXA_PICPA
HYPOTHETICAL 195.1 KD	HYPOTHETICAL 67.7 KD P	ZINC FINGER PROTEIN 13	LATE EMBRYOGENESIS ABU	CAPM PROTEIN.	36.7 KD PROTEIN IN CBR	HYPOTHETICAL 33.2 KD P	CHROMOSOME SEGREGATION	HYPOTHETICAL 117.4 KD	STE6 PROTEIN.	HPR1 PROTEIN.	VERY HYPOTHETICAL 21.7	INSERTION ELEMENT IS91	INSERTION ELEMENT IS91	CENTROMERIC PROTEIN E	DNA-DIRECTED RNA POLYM	PROBABLE ZINC PROTEASE	HYPOTHETICAL 104.8 KD	MEDIAN BODY PROTEIN.	HYPOTHETICAL 76.2 KD P	PEROXISOME ASSEMBLY PR
5.97e+01 5.97e+01	5.97e+01	5.97e+01	5.97e+01	٠	5.97e+01	5.97e+01	3.93e+01			3.93e+01	3.93e+01	3.93e+01	3.93e+01	2.56e+01					2.56e+01	

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PTHY_BOVIN
                                                                                                                                                                                                                                                                     MEDLINE; 83105964.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
WEAVER C.A., ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE; 80056GH.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

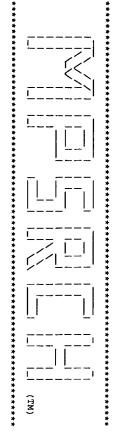
KKONDENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTH.

BOS TAURUS (BOVINE).

BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
SEQUENCE OF 32-115. MEDLINE; 71063634.
                                                                                                                                       SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T.,
COHN D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                       SEQUENCE OF 32-115.
MEDLINE; 71076182.
NIALL H.D., KEUTMANN H.T., SA
AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CH
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE 84262483.
WEAVER C.A. GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 82037785.
WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                            PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                     SAUER R., HOGAN M.L., DAWSON B.F.,
                                           CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA.
                                                                                                                                                        POTTS J.T. JR.,
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 09:57:51 1998; MasPar time 6.04 Seconds 25.396 Million cell updates/seconds

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68

Sequence: 1 SVSEIQLMHN 10

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.093; Variance 66.058; scale 0.244

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

esult No.	Score	Query Match	Length	DB DB	IJ	Description	Pred. No
1	68	100.0	34	22	W17954	Human parathyroid hor	6.37e+00
N	68	100.0	34	22	W17955		٠
ω	83	100.0	34	22	W17950	Human PTH analogue [C	6.37e+00
4	68	100.0	34	22	W20006	Cyclised human parath	6.37e+00
5	68	100.0	34	7	R34366	Human parathyroid hor	6.37e+00
σ	68	100.0	34	7	R34362	Human parathyroid hor	6.37e+00
7	68	100.0	34	20	W14310	Cyclic parathyroid ho	6.37e+00
8	83	100.0	34	20	W14309	Cyclic parathyroid ho	6.37e+00
9	83	100.0	34	22	W17947	Human parathyroid hor	6.37e+00
10	83	100.0	34	7	R34365		6.37e+00
11	68	100.0	34	7	R34364	Human parathyroid hor	6.37e+00
12	68	100.0	34	7	R34356	Human parathyroid hor	6.37e+00
13	89	100.0	34	9	R58228	[D-Asp30]-hPTH(1-34)-	6.37e+00
4	68	100.0	36	9	R58301	[NMeAla36]-hPTH(1-36)	6.37e+00
٦,	83	100.0	36	9	R58298	[NMeVal35]-hPTH(1-36)	6.37e+00
16	68	100.0	36	o	R58276	[Met(02)18]-hPTH(1-36	6.37e+00
17	83	100.0	36	Q	R58275	[Ala16]-hPTH(1-36)-NH	6.37e+00
18	68	100.0	36	9	R58242	[Lys(Isopropyl)13]-hP	6.37e+00
19	68	100.0	36	9	R58191	[Ala34]-hPTH(1-36)-NH	6.37e+00

Query Match 100.0%; Best Local Similarity 100.0%;

Score Pred.

No.

DB 22; 6.37e+00;

Length 34;

68 100.0 36 9 R58278 [Ala25] -hpTH(1-36) NH 68 100.0 36 9 R58280 [Ala26] -hpTH(1-36) NH 68 100.0 36 9 R58284 [D-Trp23] -hpTH(1-36) N 68 100.0 36 9 R58284 [D-Trp23] -hpTH(1-36) N 68 100.0 36 9 R58284 [D-Th12] -hpTH(1-36) N 68 100.0 36 9 R58284 [D-Ser3] -hpTH(1-36) N 68 100.0 36 9 R58287 [D-Ser3] -hpTH(1-36) N 68 100.0 36 9 R58287 [Ph25] -hpTH(1-36) N 68 100.0 36 9 R58287 [Ph25] -hpTH(1-36) N 68 100.0 36 9 R58287 [Ph25] -hpTH(1-36) N 68 100.0 36 9 R58289 [Lys25] -hpTH(1-36) N 68 100.0 36 9 R58249 [D-Ser1] -hpTH(1-36) N 68 100.0 36 9 R58249 [D-Ser1] -hpTH(1-36) N 68 100.0 36 9 R58244 [Ala0] -hpTH(1-36) N 68 100.0 36 9 R58244 [Ala0] -hpTH(1-38) N 68 100.0 37 9 R58244 [Ala0] -hpTH(1-38) N 68 100.0 38 9 R58131 [GJY9] -hpTH(1-38) O 68 100.0 38 9 R58131 [GJY9] -hpTH(1-38) O 68 100.0 38 9 R58105 [Val14] -hpTH(1-38) O 68 100.0 38 9 R58109 [Th13] -hpTH(1-38) O 68 100.0 44 26 P30015 Human parathyroid hor f 68 100.0 47 25 W21946 Fusion protien comprision c	45	44	43	42	41	40	39	38	37	36	35	34	ω 3	32	31	30	29	28	27	26	25	24	23	22	21	20
.0 36 9 R58278 [D-Met]8]-hpTH(10 36 9 R58290 [Ala25]-hpTH(10 36 9 R58290 [Ala26]-hpTH(10 36 9 R58284 [D-Txp23]-hpTH(10 36 9 R58284 [D-Gal6]-hpTH(10 36 9 R58264 [D-Gal6]-hpTH(10 36 9 R58284 [D-Ser]-hpTH(10 36 9 R58287 [phe25]-hpTH(10 36 9 R58288 [Lys25]-hpTH(10 36 9 R58288 [Lys25]-hpTH(10 36 9 R58249 [D-Ser]-hpTH(10 36 9 R58249 [D-Ser]-hpTH(10 36 9 R58274 [Ala15]-hpTH(10 36 9 R58214 [Ala15]-hpTH(10 36 9 R58214 [Ala19]-hpTH(10 36 9 R58214 [Clys]-hpTH(10 36 9 R58131 [Clys]-hpTH(10 38 9 R58077 [Thr13]-hpTH(10 38 9 R58077 [Thr13]-hpTH(10 38 9 R58079 [Thr13]-hpTH(10 38 9 R58097 [Thr13]-hpTH	68	68	68	68	68	68	8	68	68	68	83	68	68	68	83	68	68	68	83	83	68	68	68	68	68	68
9 R58278 [D-Met18]-hpTH(1-9 R58289 [Ala25]-hpTH(1-9 R58290 [D-Trp23]-hpTH(1-9 R58284 [D-Trp23]-hpTH(1-9 R58260 [D-Val2]-hpTH(1-9 R58284 [D-Ser3]-hpTH(1-9 R58287 [Ph25]-hpTH(1-9 R58287 [Ph25]-hpTH(1-9 R5824 [D-Ser1]-hpTH(1-9 R5824 [Ala5]-hpTH(1-3 R58274 [Ala5]-hpTH(1-3 R58274 [Ala5]-hpTH(1-3 R58274 [Ala5]-hpTH(1-3 R58274 [Ala5]-hpTH(1-3 R58131 [G119]-hpTH(1-3 R58131 [G119]-hpTH(1-3 R58105 [Tail4]-hpTH(1-9 R58105 [Tail4]-hpTH(1-9 R58077	•	•	•			•	•				•	•		•		•	٠		٠	8	8	8	00.	8	00	8
9 R58278 [D-Met18]-hpTH(1-9 R58289 [Ala25]-hpTH(1-9 R58294 [D-Trp23]-hpTH(1-9 R58284 [D-Trp23]-hpTH(1-9 R58260 [D-Val2]-hpTH(1-9 R58234 [D-Ser3]-hpTH(1-9 R58287 [Ph25]-hpTH(1-9 R58287 [Ph25]-hpTH(1-9 R5824 [D-Ser1]-hpTH(1-9 R5824 [Ala5]-hpTH(1-3 R58274 [Ala5]-hpTH(1-3 R58274 [Ala5]-hpTH(1-3 R58274 [Ala5]-hpTH(1-3 R5813] [Gly3]-hpTH(1-3 R58131 [Gly3]-hpTH(1-3 R58131 [Gly3]-hpTH(1-3 R58077 [Thr13]-hpTH(1-9 R58077	229	84	84	84	47	44	38	ა 8	38	3 8	38	37	37	36	36	36	36	36	36	36	36	36	36	36	36	36
[D-Met18]-hpTH(1- [Ala25]-hpTH(1- [Ala25]-hpTH(1- [Ala25]-hpTH(1- [D-Trp23]-hpTH(1- [D-GL16]-hpTH(1- [D-GL16]-hpTH(1- [Phe25]-hpTH(1- [Phe25]-hpTH(1- [Lys25]-hpTH(1- [Ala1]-hpTH(1- [Thx13]-hpTH(1- [Thx13]-hpTH(1- [Thx14]-hpTH(1- [Thx14]-h	9	4	ű	7	Š	õ	9	ဖ	Ø	9	9	ر.	9	ဖ	8	φ	ဖ	ဖ	ø	ဖ	9	9	9	9	9	ø
D-Met18]-hpTH(1- Ala25]-hpTH(1- Ala25]-hpTH(1- Ala26]-hpTH(1- D-Val2]-hpTH(1- D-Cala6]-hpTH(1- D-Cala6]-hpTH	R47971	R23790	W29420	W25687	W21946	P30015	R58109	809	R58077	R58105	R58131	Æ24778	R58244	27	ŝ	R58249	R58288	R58287	R58234	R58198	R58264	R58260	R58284	R58290	R58289	R58278
	equence of a full-1	hormone	parathyroid		protien con	parathyroid	]-hPTH(1-38)	3]-hPTH(1-38)	3]-hPTH(1-38)-	4]-hPTH(1-3	9]-hPTH(1-3	1-37)-amide	-hPTH(1-3	]-hpTH(1-	1-(hPTH 3	_] -hPTH(1	-hPTH(1-36	]-hPTH(1-36)-	-hPTH(1-36)	8]-hPTH(1-36	6]-hPTH(1-36	2]-hPTH(1-36	23]-hPTH(1-:	-hPTH(1-36	-hPTH(1-36)-	8]-hPTH(1-36

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WO9702834-A1.
30-JAN-1997.
03-JUL-1995; US-001105.
13-JUL-1995; US-001305.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
                                                                          The present sequence is a specific example of a human parathyroid hormone (hprH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 is alpha-aminoisobutyric acid (Aib). In this example the Glu residue at position 19 of the wild-type has been substituted by Aib. The hPrH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and
                                                                                                                                                                                     bone fracture
Claim 11; Page -; 33pp; English.
The present sequence is a specif
                                                                                                                                                                                                                           Dong 2X; WPI; 97-118819/11.

New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis
   N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim. Sequence 34~\mathrm{AA};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Aib19]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W17954;
29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W17954 standard; peptide;
                                                                calcitonin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fracture.
1 in
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                          'label- Aib
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Why; 97-18819/11.

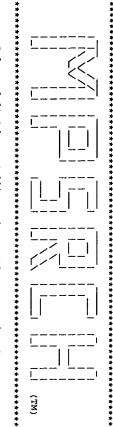
Why; 97-18819/11.

Whey variants of human parathyroid hormone 1-34 peptide - which per New variants of human parathyroid for treatment of osteoporosis and per bone fracture

PS Claim 11; Page -; 33pp; English.

CC hormone (hprH) analogue from fragment 1-34 in which at least one conjunction acid residues at positions 3, 12, 16, 17, 19 and 34 consisted and the which at least one conjunction of the wild-type has been substituted by Aib. The hPTH conjunction with anti-resorptive therapy (bisphosphonates and conjunction with anti-resorptive therapy (bisphosphonates and coarsesponds to the known hPTH 1-34 fragment with the modification. It corresponds to the known hPTH 1-34 fragment with the modifications coastated in the claim.

So Sequence 34 AA;
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                                                                                                     uery Match 100.0%;
est Local Similarity 100.0%;
Matches 10; Conservative
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03-JUL-1996; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UT 2
W17955 standard; peptide; 34
W17955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Aib34]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9702834-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                  1 svseiqlmhn 10
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1 SVSEIQLMHN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Aib
/note= "In amide form"
                                                                                                        Score 68; DB 22; Le
Pred. No. 6.37e+00;
0; Mismatches 0;
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                                                                                                                                 Length 34;
                                                                                                            Indels
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                                                                                                            0;
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                                                                                                           Gaps
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                                                                                                            0;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: bular output not generated. Thu Jul 30 09:57:07 1998; MasPar time 3.27 Seconds 111.690 Million cell updates/sec

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-1 (1-10) from US08817547A.pep 68 1 SVSEIQLMHN 10

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 22.419; Variance 28.455; scale 0.788

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

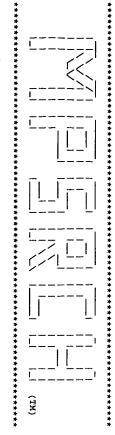
## SUMMARIES

Sult No.	Score	Query	Length	8	ID	Description	Pred. No.
-	68	100.0	34	S	1ZWA	parathyroid hormone (	4.43e-04
2	68	100.0	37	ហ	1HPH	roid	4.43e-04
ω	68	100.0	115	Н	DHIL	hormone	4.43e-04
4	68	100.0	115	_	PTPG	hormone	4.43e-04
ر ن	66	97.1	115	N	A05091	hormone	1.32e-03
σ	64	94.1	36	Ŋ	1ZWB	hormone	3.87e-03
7	64	94.1	105	N	I51851	parathyroid hormone -	3.87e-03
8	63	92.6	119	N	A34937	parathyroid hormone p	6.60e-03
9	61	٠	115	N	JC4202	parathyroid hormone -	1.89e-02
10	59	86.8	37	G	1ZWC	parathyroid hormone (	5.34e-02
11	59	•	115	Н	PTBO	parathyroid hormone p	5.34e-02
12	57	83.8	34	υ	1HTH	5	1.48e-01
13	57		35	ر.	12WD	parathyroid hormone (	1.48e-01
14	53		34	տ	1ZWE	parathyroid hormone (	1.07e+00
15	53	77.9	34	ഗ	12WG	parathyroid hormone 4	1.07e+00
16	53		34	S	12WF	_	1.07e+00
17	50		383	N	B42377	acetylornithine deace	4.47e+00
18	48	70.6	448	N	S76701	hypothetical protein	1.12e+01
19	48	70.6	1015	N	S55474	Human giant larvae ho	1.12e+01
20	47	69.1	108	N	S23204	retinol-binding prote	1.77e+01
21	47	69.1	176	2	S27192	retinol-binding prote	1.77e+01
22	46	67.6	445	N	B40970		2.76e+01
23	46	67.6	843	N	A40970	undulin 1 - human (fr	2.76e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
44	44	44	44	44	44	44	45	45	45	45	<b>4</b> 5	45	45	45	45	45	45	45	46	46	46
64.7	64.7	64.7	64.7	64.7	64.7		•	•	•	•	66.2	•		66.2	•	66.2	•	•	•	•	•
610	557	553	542	508	490	338	494	444	405	393	324	209	177	177	177	176	175	152	2163	1371	1034
N	ب	۳,	N	ш	N	سر	N	N	N	Н	Н	ب	2	Н	N	N	N	N	N	N	٨
A49082	TLBPT3	TLBPF7	S56651	A43713	S71776	JGECT	S64386	PC4436	E64995	GIMSM	GIMS	PTHU3L	JC4201	PTHU2L	A30012	S10202	JN0103	S14236	S50675	S77521	536/58
calcium-dependent pro	tail fiber protein -	tail fiber protein -	o.	calcium-dependent pro	calcium-dependent pro		pre-mRNA splicing pro	monoclonal antibody 1	othetic	gamma-1	Ig gamma-1 chain C re	parathyroid hormone-r			parathyroid hormone-1	parathyroid hormone-r	н	Ig gamma-1 chain C re	pre-mRNA splicing hel	O	mgii protein - mouse
6.57e+01	6.57e+01	6.57e+01	6.57e+01	6.57e+01		6.57e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	2.76e+01	2.76e+01	2./be+Ul

RESULT 2 ENTRY TITLE ORGANISM REFERENCE #authors #submission #cross-refer COMMENT Reserved Dete COMMENT R-va KEYWORDS FEATURE 6-9	5-9 19-30 SUMMARY Query Match Best Local Si Matches 10 Db 1 SVSEI	THE NCE SM NCE SM NCE CHOIS OK
ULT 2  IHPH #type complete RY parathyroid hormone fragment 1 37 (hpth(1-37)) (NMR, 10  structures) - synthetic  ANISM #formal_name synthetic  ERENCE A65802  #authors Marx, U.C.; Roesch, P. #submission submitted to the Brookhaven Protein Data Bank, February 1995 #cross-references pDB:IHPH #cross-references pDB:IHPH MENT Resolution: not applicable MENT Resolution: not applicable Determination: NMR MENT R-value: no refinement WORDS hormone #region helix (right hand alpha)\\ 6-9 #region helix (right hand alpha)\\	#region helix (right hand alpha)  #region helix (right hand alpha)  #region helix (right hand alpha)  #length 34 #molecular-weight 4118 #checksum 5629  ttch 100.0%; Score 68. DB 5; Length 34;  al Similarity 100.0%; Pred. No. 4.43e-04;  10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  SVSEIQLMHN 10  SVSEIQLMHN 10  Freq. No. 4.43e-04;  SVSEIQLMHN 10	12WA #type complete parathyroid hormone (residues : S HPTH(1-34) structure of human parathyroid structures #formal_name Homo sapiens #comu A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Pronces PDB:12WA TN001717 Marx, U.C. submitted to the Brookhaven Pronces PDB:12WA TN001717 Marx, U.C. in Strukturen Verschiedener Paipp.0, Bayreuth: University colution: not applicable ermination: NMR

Thu Jul 30 13:37:52 1998



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 09:55:44 1998; MasPar time 2.16 Seconds 116.271 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-1 (1-10) from US08817547A.pep 68 1 SVSEIQLMHN 10

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.348; Variance 23.508; scale 0.993

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Sult No.	Score	Query Match	Length	BB	Ħ	Description	Pred. No.
1	68	100.0	115	ъ	PTHY_HUMAN	PARATHYROID HORMONE PR	9.25e-06
2	68	100.0	115	μ		HORMONE	. 25
ω	66	97.1	115	<b>ب</b> سو	PTHY_RAT	PARATHYROID HORMONE PR	3.53e-05
4	63	92.6	119	ب	PTHY_CHICK	PARATHYROID HORMONE PR	٠
S	61	89.7	115	Ь	PTHY_CANFA	PARATHYROID HORMONE PR	.17e-
σ	59	86.8	115	,_	PTHY_BOVIN	PARATHYROID HORMONE PR	3.25e-03
7	50	73.5	369	_	PROB_CORGL	GLUTAMATE 5-KINASE (EC	
8	50	73.5	383	مبز	ARGE_ECOLI	ACETYLORNITHINE DEACET	
9	47	69.1	176	μ.	RET1_ONCMY	PLASMA RETINOL-BINDING	
10	47	69.1		μ.	RET2_ONCMY	PLASMA RETINOL-BINDING	3.65e+00
11	47			<b></b>	Y413_ARATH	HYPOTHETICAL 48.8 KD P	
12	46	67.6	2163	μ	BRR2_YEAST	PRE-MRNA SPLICING HELI	6.23e+00
13	45		175	_	PTHR_MOUSE	PARATHYROID HORMONE-RE	1.05e+01
14	45		176	ب	PTHR_CHICK	PARATHYROID HORMONE-RE	1.05e+01
15	45		177	<u>, .</u>	PTHR_RAT	PARATHYROID HORMONE-RE	1.05e+01
16	45		177	<u>ب</u>	PTHR_CANFA	PARATHYROID HORMONE-RE	1.05e+01
17	45		177	۲	PTHR_HUMAN	PARATHYROID HORMONE-RE	1.05e+01
18	45		324	_	GC1_MOUSE	IG GAMMA-1 CHAIN C REG	1.05e+01
19	45		393	_	GC1M_MOUSE	IG GAMMA-1 CHAIN C REG	1.05e+01
20	45		494	Н	PR31_YEAST	PRE-MRNA SPLICING FACT	
21	44		151	در	LE14_GOSHI	LATE EMBRYOGENESIS ABU	1.76e+01
22	44	64.7	267	1	DHPS_STAHA	DIHYDROPTEROATE SYNTHA	1.76e+01
23	44	64.7	338	ч	CYSP_SALTY	THIOSULFATE-BINDING PR	1.76e+01

45	44	43	42	41	40	39	38	37	36	35	34	ယ	32	31	30	29	28	27	26	25	24
42	42	42	42	43	43	43	43	43	43	43	43	43	43	43	44	44	44	44	44	44	44
61.8						•	63.2		•					63.2	64.7	64.7	64.7	64.7	64.7	64.7	64.7
2345	1967	551	312	1436	1136	1134	1069	870	842	651	537	444	295	103	610	557	553	542	534	508	338
Ь	ш	Н	Ь	Н	Ь	ب	Н	Ц	μ	ш	ш	س	ᆫ	μ	μ	ш	ш	_	ب	_	۲
COAC_RAT	YG50_YEAST	Y275_HAEIN	Y085_MYCPN	WC11_BOVIN	TIE1_BOVIN	TIE1_MOUSE	ENTK_MOUSE	COPG_CAEEL	AMPN_LACDL	YHJK_ECOLI	AREH_SCHPO	PGL2_ARATH	LPLC_BACSU	YF17_HAEIN	CDP1_ARATH	VTFP_BPT3	VTFP_BPT7	CDP3_ORYSA	CDP1_ORYSA	CDPK_SOYBN	CYSP_ECOLI
ACETYL-COA CARBOXYLASE	PUTATIVE RNA HELICASE	HYPOTHETICAL PROTEIN H	HYPOTHETICAL PROTEIN M	ANTIGEN WC1.1.	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	ENTEROPEPTIDASE (EC 3.	PROBABLE COATOMER GAMM	AMINOPEPTIDASE N (EC 3	HYPOTHETICAL 73.1 KD P	PROBABLE STEROL O-ACYL	EXOPOLYGALACTURONASE C	LPLC PROTEIN.	HYPOTHETICAL PROTEIN H	CALCIUM-DEPENDENT PROT	TAIL FIBER PROTEIN.	TAIL FIBER PROTEIN.	CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	THIOSULFATE-BINDING PR
4.76e+01	4.76e+01	4.76e+01	4.76e+01	2.91e+01	2.91e+01		2.91e+01		2.91e+01	2.91e+01				2.91e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01

# US-08-817-547A-1.rsp

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MEDLINE: 75146516.

MIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;

KEUTINANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;

BIOCHEMISTRY 14:1842-1847(1975).
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SYNTHESIS OF 32-65.

REDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN J.L.H., POTTS J.,

KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., 1974).

KEUTMANN H.T., PARSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMIANT ARG-18.

RA VARIANT ARG-18.

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A., ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE THE SALTS IN RANGED A., H.M.;

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE THE SALTS IN RANGED A., H.M.;

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE THE SALTS IN RANGED A., H.M.;

RA ARNOLD A., H.M.;

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MEDLINE: 73227467.

ANDREATTA R.H., HARTWANN A., JOEHL A.,

ANDREATTA R.H., SIEBER P.;

RINIKER B., RITTEL W., SIEBER P.;

RINIKER B., RITTEL W.,

RINIKER B., RINIKER B.,

RINIKER B., RITTEL W.,

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RINIKER B.,
                                                                                                                                                                STRUCTURE BY NMR OF 32-65.
STRUCTURE; 91299748.
MEDLINE; 91299748.
T., WRAY V., SCHOMBURG D., WINGENDER E.,
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 32-65.

STRUCTURE; 93345518.

MEDLINE; 93345518.

BARDEN J.A.; CUTHBERTSON R.M.;

BARDEN J.A.; CUTHBER 5315-321(1993).

EUR. J. BIOCHEM. 215:315-321
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MEDLINE: 95318084.
MEDLINE: 95318084.
MOSTERVANN S., BAYER P., ADERWANN K.,
MARX U.C., AUSTERVANN S., SCHMID F.-X., JAENICKE R.,
STICHT H., WALTER S., SCHMID F.-X.,
STICHT H., WALTER S., SCHMID F.-X.,
STICHT H., WALTER S., SCHMID F.-X.,
STICHT H., WALTER S., SCHMID F.-X., JAENICKE R.,
ROESCH P., WALTER S., SCHMID F., STICHT H.,
ROESCH P., WALTER S., SCHMID F., WALTER S., SCHMID F., WALTER S., WALTER
100.0%; Query Match similarity 100.0%; Best Local Similarity 200.0%; Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOL. CHEM. 270:15194-15202(1995).
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SEQUENCE
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PARATHYROID; 1. 3D-STRUCTURE.

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Score No. 9.25e-06;
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O; Mismatches O;
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C -> R (IN FIH; LEADS TO INEFFICIENT
C -> R (IN FIH; PRECURSOR).
PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
143E87C7 CRC32;
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FORSSMANN
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01-FEB-1996 (
PARATHYROID H
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SEQUENCE FROM N.A.
MEDLINE; 87316938.
MEDLINE; 87316938.
SCHMELZER H.-J., GRC
SCHMELZER H.-J., GRC
NUCLEIC ACIDS RES. 1
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EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA;
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SECUENCE OF 26-115.
MEDLINE; 76018954. -Y., LITTLEDIKE E.T., HAMILTON J.W., CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W., BIOCHEMISTRY 14:3631-3635(1975).
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BIOCHEMISTRY 13:1994-1999(1974).

1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS CALCIUM LEVEL BY DISSOLVING THEIR RENAL EXCRETION.

1- FUNCTION: PROSTITE; PEPG.

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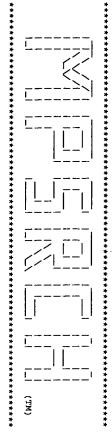
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O'RIORDAN J.L.H.,

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 09:56:12 1998; MasPar time 3.80 Seconds 110.885 Million cell updates/secondar output not generated.

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68
Sequence: 1 SVSEIQLMHN 10
Scoring table: PAM 150

Scoring table: PAM 150
Gap 15
Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl5

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.590; Variance 21.849; scale 1.034

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

200 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Score
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Gaps	ACETYLGLUTAMATE KINASE (EC 2.7.2 ARGB. LACTOBACILLUS PLANTARUM. PROKARYOTA; FIRMICUTES; REGULAR ! [1] SEQUENCE FROM N.A. STRAIN-CCM 1904; BRINGEL F., FREY L., BOIVIN S., I J. BACTERIOL. 179:0-0(1997).	O08320; 01-JUL-1997 (TREMBLREL 04, CREATED) 01-JUL-1997 (TREMBLREL 04, LAST SEQUENCE 01-JAN-1998 (TREMBLREL 05, LAST ANNOTATI	SULT 2	Db 22 AISEIQLMHN 31 ::        Qy 1 SVSEIQLMHN 10	Query Match 94.1%; Score 64; DB 10; Length 105; Best Local Similarity 80.0%; Pred. No. 5.68e-05; Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps	RY [1]  RP SEQUENCE FROM N.A.  RC TISSUE-THYROID, AND PARATHYROID;  RA SCHMELZER H.J., GROSS G., MAYER H.;  RL ADV. GENE TECHNOL. 21:228-229(1984).  DR EMBL; M54875; G601933;  FT NON_TER 1 1  SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;		RESULT 1 ID 063473 PRELIMINARY; PRT; 105 AA.
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March completed: Thu Jul 30 09:56:47 1998 Job time : 35 secs.
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SDEQUENCE FROM N.A.
SERAIN-CCM 1904;
STRAIN-CCM 1904;
BRINGEL F.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
FORMALYTIC ACTIVITY; ATP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.
ADP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.
EMBL; X99978; E284231; TANNSFERASE.
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SEQUENCE 248 AA; 26580 MW; 3E945D79 CRC32;
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Query Match 100.0%; Score 63; DB 22; Length 34; Best Local Similarity 100.0%; Pred. No. 9.63e+00;

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RESULT
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pri Dong ZX;

New variants of human parathyroid hormone 1-34 peptide - which pri stimulate bone growth and are used for treatment of osteoporosis and pri stimulate bone growth and are used for treatment of osteoporosis and pri bone fracture;

pri and 34

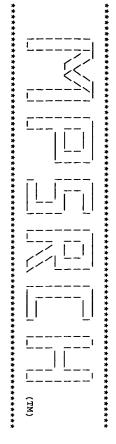
cc at position 34 of the wild-type has been substituted by Aib. The hPTH

cc at position 34 of the wild-type has been substituted by Aib. The hPTH

cc analogues stimulate bone growth and so are useful in human or veterinary

cc analogues stimulate bone growth and so are useful in human or veterinary

cc conjunction with anti-resorptive therapy (bisphosphonates and conjunction with anti-resorptive therapy
Search completed: Thu Jul 30 10:00:14 1998 Job time : 16 secs.
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W17955; standard; peptide; 34 AA.
W17955; lfirst entry)
29-UUL-1997 (first entry)
Human parathyroid hormone analogue [Aib34]hpTH(1-34)NH2.
Steepporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.
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30-JAN-1997.
03-JUL-1996; U11292.
03-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-625186.
29-MAR-1996; US-625186.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 09:59:20 1998; MasPar time 3.14 Seconds 104.825 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-817-547A-2 (1-9) from US08817547A.pep 63 1 SVSEIQLMH 9

bular output not generated.

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.980; Variance 26.868; scale 0.818

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

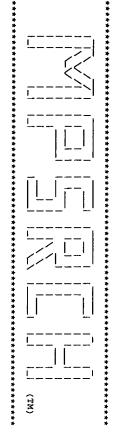
No.	Score	Match	Length	DB	IJ	Description	Pred. No.
H .	63	100.0	34	5	1ZWA	parathyroid hormone (	2.58e-03
N	63		37	σ	1HPH		.58e-
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4	63	100.0	115	ب	PTPG	hormone	2.58e-03
տ	61	96.8	115	N	A05091	parathyroid hormone p	.78e-
0	59	93.7	36	ഗ	1ZWB	parathyroid hormone (	2.31e-02
7	59	93.7	105	N	151851	parathyroid hormone -	2.31e-02
œ	58	92.1	119	N	A34937	parathyroid hormone p	3.94e-02
9	56	88.9	115	N	JC4202	parathyroid hormone -	1.14e-01
10	54	85.7	37	Ç	1ZWC	parathyroid hormone (	3.21e-01
11	54	85.7	115	$\vdash$	PTBO	parathyroid hormone p	3.21e-01
12	52	82.5	34	S	1HTH	cyclic parathyroid ho	.88e-
13	52	82.5	35	ر.	1ZWD	roid	8.88e-01
14	48	76.2	34	U	1ZWE	parathyroid hormone (	6.33e+00
15	48	76.2	34	u	1ZWG	parathyroid hormone 4	6.33e+00
16	48	76.2	34	ഗ	12WF	parathyroid hormone 4	6.33e+00
17	48	76.2	1015	N	S55474	Human giant larvae ho	6.33e+00
18	47	74.6	383	N	B42377	acetylornithine deace	1.02e+01
19	47		448	N	S76701	hypothetical protein	1.02e+01
20	46		445	N	B40970	1 54	1.62e+01
21	46		843	N	A40970	undulin 1 - human (fr	1.62e+01
22	46	73.0	1034	N	S36758	mgl1 protein - mouse	1.62e+01
23	45	71.4	152	N	S14236	hai	2.57e+01

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
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66.7	66.7	66.7	66.7		68.3						68.3						69.8	71.4	71.4	71.4	71.4
619	579	176	176	116	2163	1136	1134	1057	651	402	247	225	167	103	557	553	99	1371	444	393	324
N	N	N	N	N	N	μ		N	N	N	N	N	N	N	ب	μ	2	N	2	ب	ப
159558	S54872	S10202	S27192	S22553	S50675	S57845	JN0711	138171	S47750	S76629	S60307	S77105	E69768	D64034	TLBPT3	TLBPF7	C64489	S77521	PC4436	GIMSM	G1MS
dopamine transporter	penicillin-binding pr	parathyroid hormone-r	inol-binding p	Ig heavy chain V regi	pre-mRNA splicing hel	protein-tyrosine kina	protein-tyrosine kina	hugl protein - human	hypothetical protein	hetical pr	3	hypothetical protein		hypothetical protein	tail fiber protein -	tail fiber protein -	hypothetical protein	sensory transduction	monoclonal antibody 1	Ig gamma-1 chain C re	Ig gamma-1 chain C re
9.79e+01	9.79e+01	9.79e+01	9.79e+01	9.79e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	4.05e+01	4.05e+01	4.05e+01	2.57e+01	2.57e+01	2.57e+01	2.57e+01

RESULT 2 ENTRY TITLE ORGANISM REFERENCE #authors #submission #cross-refer COMMENT Reso. COMMENT Dete: COMMENT PRESO. COMMENT Reso. COMMENT PRESO. COMMENT Reso.	Query Match Best Local Similarity Matches 9; Conser Db 1 SVSEIQLMH 9                     Qy 1 SVSEIQLMH 9	, o . w .	#SUDDISSION SUB- #SUDDISSION SUB- #CTOSS TEFERENCE TNO! #AUTHORS MAT: #BOOK In: #BOOK PPI COMMENT Resolution	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE REFERENCE
ULT 2  IHPH #type complete RY parathyroid hormone fragment 1 37 (hpth(1-37)) (NMR, 10  Structures) - synthetic  ANISM #formal_name synthetic  ERENCE A65802  #authors Marx, U.C.; Roesch, P. #submission submitted to the Brookhaven Protein Data Bank, February 1995 #cross-references PDB:IHPH MENT Resolution: not applicable MENT Resolution: not applicable MENT Determination: NMR MENT Determination: no refinement WORDS hormone TURE TURE  #region helix (right hand alpha)\ 6-9 #region helix (right hand alpha)\	100.0%; Score 63; DB 5; Length 34; similarity 100.0%; Pred. No. 2.58e-03; 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; IOLMH 9	Determination: NMR hormone  #region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629	ion submitted to the Brookhaven Protein Data Bank, June 1996 eferences PDB:1ZWA TN001717 Marx, U.C. Marx, U.C. In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: not applicable	12WA #type parathyroid hormo HPTH(1-34) Structure of huma structures #formal_name Homo A67856

Page 2

	Search completed: Thu Jul 30 09:59:39 1998 Job time : 19 secs.	Db 1 SVSEIQLMH 9 Qy 1 SVSEIQLMH 9	#region helix (right hand alpha) 17-28 #length 37 #molecular-weight 4401 #checksum 3791 SUMMARY 100.0%; Score 63; DB 5; Length 37; Query Match Best Local Similarity 100.0%; Pred. No. 2.58e-03; Indels 0; Gaps 0; Matches 9; Conservative 0; Mismatches 0; Indels 0



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:58:20 1998; MasPar time 2.06 Seconds 109.762 Million cell updates/sec

bular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-2 (1-9) from US08817547A.pep 63 1 SVSEIQLMH 9

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.879; Variance 22.094; scale 1.036

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	63	100.0	115	μ	PTHY_HUMAN	PARATHYROID HORMONE PR	7.43e-05
N	63	100.0	115	ب	1 1	HORMONE	7.43e-05
ω	61	٠	115	μ	PTHY_RAT	PARATHYROID HORMONE PR	. 88e
4	58	92.1	119	<u>س</u>	PTHY_CHICK	PARATHYROID HORMONE PR	e-
ر ن	56	•	115	μ.,	PTHY_CANFA	PARATHYROID HORMONE PR	.69e-
6	54	•	115	4	PTHY_BOVIN	PARATHYROID HORMONE PR	3e-C
7	50	79.4	369	щ	PROB_CORGL	GLUTAMATE 5-KINASE (EC	.16e
00	47	74.6	383	<b>j</b>	ARGE_ECOLI	ACETYLORNITHINE DEACET	ċ
Q	47	74.6	435	μ	Y413_ARATH	HYPOTHETICAL 48.8 KD P	1.81e+00
10	45	71.4	324	ب	GC1_MOUSE	IG GAMMA-1 CHAIN C REG	5.55e+00
11	45	71.4	393	_	GC1M_MOUSE	IG GAMMA-1 CHAIN C REG	5.55e+00
12	44	69.8	151	Н	LE14_GOSHI	LATE EMBRYOGENESIS ABU	9.57e+00
13	44	69.8	553	Н	VTFP_BPT7		9.57e+00
14	44	69.8	557	μ	VTFP_BPT3	TAIL FIBER PROTEIN.	9.57e+00
15	43	68.3	103	Ц	YF17_HAEIN	HYPOTHETICAL PROTEIN H	
16	43	68.3	651	Н	YHJK_ECOLI	HYPOTHETICAL 73.1 KD P	1.63e+01
17	43	68.3	1069	$\vdash$	ENTK_MOUSE	ENTEROPEPTIDASE (EC 3.	1.63e+01
18	43	68.3	1134	Н	TIE1_MOUSE	TYROSINE-PROTEIN KINAS	1.63e+01
19	43	68.3	1136	Н	TIE1_BOVIN	TYROSINE-PROTEIN KINAS	1.63e+01
20	43	68.3	2163	Н	BRR2_YEAST	PRE-MRNA SPLICING HELI	1.63e+01
21	42	66.7	175	$\vdash$	PTHR_MOUSE	PARATHYROID HORMONE-RE	2.76e+01
22	42	66.7	176	Н	RET1_ONCMY	PLASMA RETINOL-BINDING	2.76e+01
23	42	66.7	176	_	RET2_ONCMY	PLASMA RETINCL-BINDING	2.76e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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65.1	65.1	65.1	S	ß	5	65.1	S	G	U	ū	66.7	6	σ	σ	σ	σ	66.7	σ	σ	66.7	66.7
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RRPL_VSVSJ	YG50_YEAST	DP31_MYCPN	VIRL_AGRT6	YCCC_ECOLI	TESK_RAT	TESK_HUMAN	KRCB_HUMAN	CWLL_BACLI	Y085_MYCPN	YZ24_METJA	RRPO_NMV	COPG_CAEEL	NTDO_RAT	CDP1_ARATH	CDP3_ORYSA	CDP1_ORYSA	CDPK_SOYBN	PTHR_RAT	PTHR_HUMAN	PTHR_CANFA	PTHR_CHICK
RNA POLYMERASE BETA SU	PUTATIVE RNA HELICASE	PUTATIVE DNA POLYMERAS	LIMITED HOST RANGE (LH	HYPOTHETICAL 81.2 KD P	TESTIS-SPECIFIC PROTEI	TESTIS-SPECIFIC PROTEI	RAC-BETA SERINE/THREON	N-ACETYLMURAMOYL-L-ALA	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	RNA REPLICATION PROTEI	PROBABLE COATOMER GAMM	SODIUM-DEPENDENT DOPAM		CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	PARATHYROID HORMONE-RE	PARATHYROID HORMONE-RE	PARATHYROID HORMONE-RE	PARATHYROID HORMONE-RE
4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01		4.60e+01	4.60e+01	2.76e+01					2.76e+01	2.76e+01		2.76e+01		2.76e+01

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[7]		PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,	T. JR.;	NIALL H.I	OF 75-	BIOCHEMISTRY 17:5723-5729(1978).		H.T., SA	79082855.	UENCE		PROC. NATI. ACAD. SCI. U.S.A. 71: 384-388(1974).	SAUER R.T., JACOBS J.W., KEUIMANN		SEQUENCE OF 32-68.	[4]	249:155-157(1974).	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;		UENCE		NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983)	.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;	T.J., MCCEVITT		SEQUENCE FROM N.A.	C. NATE: ACAD: SCI. U.S.A.	G.N., KRONENBERG H.	NE; 82150870.	SEQUENCE FROM N.A.	[1]		RYOTA: ME	HOMO SADTENS (HIMAN)	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).	35, LAST ANNOTATION UPDAT	(REL. 05,	1986 (REL.	PO1270:	THY UTWAN CHANDADD. DDT. 115

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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MEDLINE: 7327467.

ANDREATTA R.H., HARTMANN A., JOEHL
ANDREATTA R.H., SIEBER P.;

RINIKER B., RITTEL W., SIEBER P.;

HELV. CHIM. ACTA 56:470-473(1973).
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MEDLINE; 75059220.

MEDLINE; 75059220.

TREGERR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.
KEUTMANN H.T., PARSONS J.A. 355:415-421(1974).
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
KEUTMANN H.T. 1842-1847(1975).
                                                                                                                                                                                                                                                             EMBL, A29146)
PIR, A01556;
PIR, A01556;
PIR, A1939;
PDB; 1HPH; 10
PDB; 1HPH; 11
PDB; 1ZWB; 12
PDB; 1ZWB; 12
PDB; 1ZWC; 16
PDB; 1
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MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
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BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
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-I DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAVERHEL; J00301; G190704; ---
EMBL; J00597; G37144; ---
EMBL; A29146; E186700; ---
PIR; A01536; PTHU.
PIR; A01536; PTHU.
PIR; A19339; A19339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARX U.C., AUSTERMANN S., BAYER P., ADERMANN K., STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., ROESCH P.;
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ARNOLD A., HORST S.A., GARDELLA T.J.,
KRONENBERG H.M.;
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-i- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
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12-MAR-97.
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15-OCT-97.
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DISEASE MUTATION;
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18
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          Score 63; DB 1; I
Pred. No. 7.43e-05;
0; Mismatches
                                                                                       PARATHYROID HORMONE.
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N -> D (IN REF. 5).
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FORSSMANN W.-G.,
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P01269;
21-JUL-1986
01-JAN-1988
01-FEB-1996
PARATHYROID
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EUKARYOTA; METAZO
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MEDLINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W.,
BIOCHEMISTRY 14:3631-3635(1975).
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EUTHERIA; ARTIODACTYLA.
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SEQUENCE OF 32-115.

MEDLINE; 74253317.

SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RI SAUER R.T., JR.;

POTTS J.T., JR.;

BIOCHEMISTRY 13:1994-1999(1974).

FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING DONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; X05722; G1839; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE; 87316938
SCHWELZER H.-J., GROSS G., WIDERA G., MAYER
SCHWELZER H.-J., GROSS G. WIDERA G., MAYER
NUCLEIC ACIDS RES. 15:6740-6740(1987).
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(REL. 06, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
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1115 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Result No. Scor	Statistics: Pred. score and is	atabas	Post-processing:	Searched:	tion: Scor e:	<pre>MPsrch_pp p in on: dbular outpu</pre>	; ; ;	• 1 •
3.7 105 10 Q 66.2 1015 2 Q 66.	SUMMARIES  Query e Match Length DB ID	results to the of the	emb15 sp_fung1 2:sp_human 3 sp_mhc 6:sp_organelle sp_bacteria 10:sp_rod :sp_unclassified	Minimum Match 0% Listing first 45 summarie	Gap 15 140542 seqs, 42109429 res	>US-08 (1-9) :: 63 1 SVSE	rotein - protein database se Thu Jul 30 09:58:46 1998 t not generated.	ease 3.1A John F. Collins, yright (c) 1993-1998 University of the control of the	
ARATHYROID HORMONE (F 6.56e CETYLGLUTAMATE KIMASE 8.60e 11ANT LARVAE HOMOLOGUE 8.60e YPOTHETICAL 49.8 KD P 1.57e NDULIN 1 (MATRIX GLYC 2.85e ETHAL GIANT LARVAE HO 2.85e EMILAR TO TYROSINE KI 5.12e TEROID RECEPTOR COACT 5.12e T	Description Pred. No.	20.804; scale 1.064  predicted by chance to have a score of the result being printed, total score distribution.	:sp_invertebrate 7:sp_phage 8:sp ent 11:sp_virus	ίδ.	idues	סי	using Smith using time 3472 Millio	mputing Researc of Edinburgh,	

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	<u>u</u>	30	29	28	27	26	25	24	23	22	21	
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	SIMILAR TO S. CEREVISI	C49F5.2.	CALMODULIN-DOMAIN PROT	PENICILLIN-BINDING PRO	CALCIUM-DEPENDENT CALM	F47A4.3.	CALMODULIN-DOMAIN PROT	CALMODULIN-DOMAIN PROT	CALMODULIN-DOMAIN PROT	CALCIUM DEPENDENT PROT	CALMODULIN-LIKE DOMAIN	CALCIUM-DEPENDENT PROT		CALCIUM-DEPENDENT PROT	NUCLEAR F		FROM BASES 2347342 TO	CONSERVED PROTEIN.	POLYPROTEIN.	TUMOUR SUPPRESSOR PROT	TERMINAL PROTEIN.	HEXON PROTEIN.	HYPOTHETICAL 45.8 KD P	AGAMOUS PROTEIN.	FBP6 PROTEIN.	
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Best Local Similarity 77.8%;
Matches 7; Conservative
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TISSUE-THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL, M54875; G60193; -.
NON_TER
NON_TER
SEQUENCE 105 AA; 11746 MW; 6AC3163.
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08320 PRELIMINARY; PRT; 248 AA.
008320;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
ACETYLGLUTAMATE KINASE (EC 2.7.2.8).
SEQUENCE FROM N.A.
STRAIN-CCM 1904;
BRINGEL F., FREY L., BOIVIN S., HUBERT J.C.;
J. BACTERIOL. 179:0-0(1997).
                                                                                                                                                                                                                                           ARGB.
LACTOBACILLUS PLANTARUM.
PROKARYOTA; FIRMICUTES; REGULAR ASPOROGENOUS ROD; LACTOBACILLACEAE.
[1]
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
[1]
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1 SVSEIQLMH 9
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105 AA; 11746 MW; 6AC3163E CRC32;
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RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-CCM 1904;

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: bular output not generated Thu Jul 30 10:02:44 1998; MasPar time 2.60 Seconds 47.195 Million cell updates/sec

Title:

Sequence: Description: Perfect Score: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SYSEIQLM 8

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.998; Variance 50.414; scale 0.298

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		% Query				
No.	Score		Length DB	ij	Description	Pred. No.
ш	54	100.0	17 1	8 R94192	Human parathyroid hor	2.22e+01
2	54	100.0	34 20	0 R99978	Human parathyroid hor	2.22e+01
ω	54	100.0	34 20	0 W01610	Parathryoid hormone a	2.22e+01
4	54	100.0	34	7 R34361	Human parathyroid hor	2.22e+01
ر ن	54	100.0	34 .	7 R34360	Human parathyroid hor	2.22e+01
6	54	100.0	34 23	3 W24276	Parathyroid hormone (	2.22e+01
7	54	100.0		3 W08130	Human PTH derivative,	2.22e+01
œ	54	100.0		3 W08131	Human PTH derivative,	2.22e+01
9	54	100.0		3 W24273	Wild type parathyroid	2.22e+01
10	54	100.0			н	2.22e+01
11	54	100.0	34 8	8 R41559		2.22e+01
12	54	100.0	N	2 W17954	Human parathyroid hor	2.22e+01
13	54	100.0		2 W17955		2.22e+01
14	54	100.0	34	7 R34359		2.22e+01
15	54	100.0	34	7 R34357	Human parathyroid hor	2.22e+01
16	54	100.0		3 R88829		2.22e+01
17	54	100.0	34 20	0 W14312	ο.	2.22e+01
18	54	100.0			Porcine parathyroid h	2.22e+01
19	54	100.0	34	8 R41565	[Arg16, Gln27]hPTH (1	

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1 svseiqlm 8 |||||||| 1 svseiqlm 8

54 100.0 34 8 R41552 [E3,116]hpFH (1-34). 54 100.0 34 9 R58189 54 100.0 34 9 R58189 54 100.0 34 7 R34368 Human parathyroid hor 54 100.0 34 22 W17952 Human parathyroid hor 54 100.0 34 23 W08114 Human parathyroid hor 54 100.0 34 22 W1994 Cyclised human parath 54 100.0 34 7 R34367 Human parathyroid hor 54 100.0 34 7 R34356 Human parathyroid hor 54 100.0 34 7 R34356 Human parathyroid hor 54 100.0 36 9 R58275 [Met(02)18]-hpTH(1-36)-NH 54 100.0 36 9 R58276 [Met(02)18]-hpTH(1-36)-NH 54 100.0 36 9 R58238 [D-8sp30]-hpTH(1-36)-NH 54 100.0 36 9 R58238 [D-8sp30]-hpTH(1-36)-NH 54 100.0 36 9 R58238 [D-8sp30]-hpTH(1-36)-NH 54 100.0 36 9 R58238 [P-83]-hpTH(1-36)-NH 54 100.0 36 9 R58238 [P-83]-hpTH(1-36)-NH 54 100.0 36 9 R58188 [P-83]-hpTH(1-36)-NH 54 100.0 36 9 R58188 [P-83]-hpTH(1-38)-OH 54 100.0 37 9 R58245 [P-00]-hPTH(1-38)-OH 54 100.0 38 9 R58143 [G1n21]-hpTH(1-38)-OH 54 100.0 44 26 P30015 54 100.0 47 25 W21946 Fusion parathyroid hor 54 100.0 84 27 W25687 Human parathyroid hor 54 100.0 84 27 W25687 Human parathyroid hor 54 100.0 84 28 W29420 Human parathyroid hor
34 8 R41552 [Glub 10] 34 9 R58189 [F23] 34 22 W17952 Human 10] 34 22 W17952 Human 10] 34 23 W08114 Human 10] 34 24 W19994 Cycl 10] 34 9 R58181 [Thr 10] 34 9 R58181 [Thr 10] 34 8 R41568 [Lye 10] 34 8 R41568 [Lye 10] 35 9 R58275 [Alta 10] 36 9 R58276 [Met 10] 36 9 R58237 [Met 10] 36 9 R58237 [D-4] 37 9 R58237 [D-4] 38 9 R58188 [D-4] 39 R58188 [Phe 10] 30 36 9 R58188 [Phe 10] 31 9 R58114 [Val 10] 32 9 R58114 [Val 10] 33 9 R58114 [Val 10] 34 25 W25407 [Human 10] 35 W25407 [Human 10] 36 9 R5817 [Human 10] 37 9 R5817 [Human 10] 38 9 R5817 [Human 10]
8 R41552 [Glu 9 R58189 [F23 22 W17952 Huma 7 R34368 Huma 23 W08114 Huma 23 W1994 Cycl 9 R58181 [Thr 7 R34356 Huma 7 R34356 Huma 8 R41568 [Lya 9 R58275 [Alab 9 R58276 [Met 9 R58237 [Dr-4 9 R58249 [Dr-4 9 R58249 [Prc 9 R58249 [Prc 9 R58245 [Prc 9 R58114 Huma 25 W219420 Huma 25 W219420 Huma 25 W23500 Porc
R41552 [Glu R58189 [F23 W17952 Huma W19952 Huma W08114 Huma W19994 Cycll R58181 [Thr R34356 Huma R34356 Huma R341568 [Lys R58275 [Alab R58276 [Met R58237 [D-8 R58237 [D-8 R58237 [D-8 R58237 [D-8 R58237 [Thr R58138 [D-8 R58249 [Prc R58249 [Prc] R58249 [
(Glu (F23) Huma Huma Cycl (Thr Huma Huma (Cycl (Thr Huma Huma (Lyy (Ala (Ala (Met H) (D-4) (Ph-6 (Ph-6 (Ph-6 (Ph-6 (F) (Val Huma Huma Fusi Stah Huma
[GLUL6] hPFH (1-34). [F23,H25,H26,L27,I28,Human parathyroid hor Human parathyroid hor [Lys15,16 His27] hPTH [1-36]. NH [Met(02)18] - hPTH(1-36) - NH [Met) hPTH(1-36) - NH [Met] hPTH(1-36) - NH [Phe23] - hPTH(1-36) - NH [Phe23] - hPTH(1-38) - OH [GL121] -

# ALIGNMENTS

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Search completed: Thu Jul 30 10:03:01 1998 Job time: 17 secs.
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PF 10-MAR-1995; DE-008672.

PF 10-MAR-1995; DE-008672.

PR (BOEF) BOEHRINGER MANNHEIM GMBH.

POORY C, ESSWein A, Hoffmann E, Honold K, Schaefer W;

PI DONY C, ESSWein A, Hoffmann E, Honold K, Schaefer W;

PI DONY C, ESSWein A, Hoffmann E, Honold K, Schaefer W;

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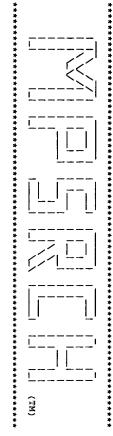
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PI DONY C, ESSWein A, Honold K, Schaefer W;

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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 2
199978 standard; peptide; 34 AA.
R99978;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:01:58 1998; MasPar time 3.10 Seconds 94.424 Million cell updates/sec

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Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SVSEIQLM 8

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.117; Variance 23.944; scale 0.882

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

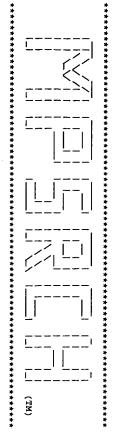
#### SUMMARIES

sult No.	Score	% Query Match	Length	BG	ID	Description	
1	54	100.0	34	5	1ZWA	parathyroid hormone (	6.75e-02
N	54		37	ហ	<b>1</b> HPH	roid	φ
w	54		115	Н	PTHU	_	6.75e-02
4	54		115	<u>, , , , , , , , , , , , , , , , , , , </u>	PTPG	hormone	٠,
5	52		115	N	A05091	hormone	2.07e-01
σ	50		36	υ	1ZWB	hormone	6.18e-01
7	50		105	N	151851	parathyroid hormone -	.18e-
œ	49		119	N	A34937	parathyroid hormone p	
9	47		115	N	JC4202	parathyroid hormone -	3.04e+00
10	45		37	U	1ZWC	parathyroid hormone (	8.50e+00
11	45		115	Н	PTBO	parathyroid hormone p	8.50e+00
12	43		34	G	1HTH	thyroid h	2.30e+01
13	43		35	σı	12WD		2.30e+01
14	43		167	N	E69768	hypothetical protein	2.30e+01
15	43		1134	μ	JN0711	m	2.30e+01
16	43		1136	Ь	S57845	protein-tyrosine kina	2.30e+01
17	41		259	N	G64512	SOJ protein homolog -	6.02e+01
18	41		260	N	A38114	resolvase rsd - Salmo	6.02e+01
19	41	75.9	312	N	S73934	MG085 homolog G07_orf	6.02e+01
20	41		312	N	S66952	prot	6.02e+01
21	41		441	N	S41710	mitosis-specific cycl	6.02e+01
22	41		481	_	A46288	protein kinase (EC 2.	6.02e+01
23	41		481	N	JC2438	tein kin	6.02e+01

45	44	43	42	41	40	39	38	37	36	ω G	34	33	32	31	30	29	28	27	26	25	24
39	39	39	39	39	40	40	40	40	40	40	40	40	41	41	41	41	41	41	41	41	41
•	٠	•		72.2	٠	74.1	74.1	74.1	74.1	74.1	74.1	74.1	75.9	75.9	75.9	75.9	75.9	75.9	75.9	75.9	75.9
402	245	34	34	34	3124	1487	1150	1061	883	353	306	99	1371	896	896	835	605	591	591	590	589
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hypothetical protein	protein hglK - Synech	parathyroid hormone 4	parathyroid hormone 4	parathyroid hormone (	collagen alpha 1(XII)	probable membrane pro	probable membrane pro	traC-1 protein - Esch	hypothetical protein	conserved hypothetica	ribonucleoside-diphos	hypothetical protein	sensory transduction	hypothetical protein	Ð	virA protein - Agroba	El protein - human pa	reduced folate carrie	reduced folate carrie		folate binding protei
1.52e+02	1.52e+02	1.52e+02	1.52e+02	1.52e+02	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+03	6.02e+03	6.02e+0

6-9	COMMENT Deter COMMENT R-val KEYWORDS FEATURE	hors miss ss-r	TITLE ORGANISM REFERENCE	RESULT 2	Qy 1 SVSEIQLM	Db 1 SVSEIQLM	Query Match Best Local Sim Matches 8;	6-9 19-30 SUMMARY	COMMENT Resol COMMENT Deter KEYWORDS FEATURE	#authors #book	#submission #cross-refere REFERENCE	ORGANISM REFERENCE #authors	ALTERNATE_NAMES PDB_TITLE	TITLE	RESULT 1
<pre>#region helix (right hand alpha)\</pre>	Determination: NMK R-value: no refinement hormone	#authors Marx, U.C.; Roesch, P. #submission submitted to the Brookhaven Protein Data Bank, February 1995 #cross-references pDB:JHPH MENT Resolution: not applicable	parathyroid hormone fragment 1 37 (hpth(1-37)) (NMR, 10 structures) - synthetic #formal_name synthetic A65802	מיס המיס של איני שני איני איני איני איני איני איני	8 MI	EM 8	<pre>/ Match 100.0%; Score 54; DB 5; Length 34; Local Similarity 100.0%; Pred. No. 6.75e-02; les 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34  #molecular-weight 4118  #checksum 5629</pre>	le	Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0. Bavreuth : University of Bavreuth (Thesis), 1996	ed to the :1ZWA 7	'#formal_name Homo sapiens #common_name man A67856 ROESCh, P.; Marx, U.C.	HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures	12WA #type complete parathyroid hormone (residues 1-34) - human	

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. n on: Thu Jul 30 10:00:33 1998; MasPar time 2.09 Seconds 95.854 Million cell updates/sec

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SVSEIQLM 8

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.952; Variance 19.669; scale 1.116

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

222 23	No.
D. D. D. G.	Score
100.0 96.3 87.0 87.0 79.6 83.3 75.9 75.9 75.9 75.9 75.9 75.9 75.9 75.9	Query Match
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4.02e-03 1.58e-02 1.16e-01 4.17e-01 4.18e-00 4.80e+00 4.80e+00 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01	Pred. No.

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CUT1 PROTEIN. RNA POLYMERASE BETA SU	ANTIGEN WC1.1.	DNA-DIRECTED RNA POLYM	TESTIS-SPECIFIC PROTEI	TESTIS-SPECIFIC PROTEI	TRANSPORT ATP-BINDING	HEAT SHOCK FACTOR PROT	SERINE PROTEASE I PREC	HEAT SHOCK FACTOR PROT	CHECKPOINT PROTEIN MEC	ORNITHINE DECARBOXYLAS	ORNITHINE DECARBOXYLAS	PROLYL-TRNA SYNTHETASE	ORNITHINE DECARBOXYLAS	TYPE 4 PREPILIN-LIKE P	GLUTATHIONE S-TRANSFER	CHLOROPLAST 30S RIBOSO	RIBULOSE-PHOSPHATE 3-E	COLLAGEN ALPHA 1(XII)	MDS3 PROTEIN (MCK1 DOS	HYPOTHETICAL 133.0 KD
4.60e+01 4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	2.66e+01	2.66e+01	2.66e+01

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REVISIONS.
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
BIOCHEMISTRY 14:1842-1847(1975).
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A KRONENBERG H.M.;
A KRONENBERG H.M.;
BOLIN. INVEST. 86:1084-1087(1990).
I. FUNCTION: PHE ELEVARES CALCIUM LEVEL BY DISSOLVING THE SALTS
HONGE AND PREVENTING THEIR RENAL EXCRETION.
I. DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
HYPOPARATHYROIDISM (FIH).
EMBL; J00301; G190704; -.
EMBL; V00507; G37144; -.
EMBL; V00507; G37144; -.
EMBL; A29146; E186700; -.
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MEDLINE; 75059220.

MEDLINE; 75059220.

MEDLINE; 75059220.

VAN RIETSCHOTEN J., GREEN E., NIALL H.D., PREGER G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D., PATSONS J.A., O'RIORDAN J.L.H., POTTS J.T. KEUTWANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95318084.
MARX U.C., AUSTERMANN S
STICHT H., WALTER S., S(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANDREATTA R.H., HARTMANN A., JOEHL A., ANDREATTA R.H., SIEBER P.; RINIKER B., RITTEL W., SIEBER P.; HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
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MEDLINE: 73227467.
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MEDLINE; 93345518.

CUTHBERTSON R.M.;

BARDEN J.A.; CUTHBERTSON P.M.;

BARDEN J.A.; CUTHBERTSON R.M.;
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                                                                                                                                                                                  PIR; A01339; A1339.
PIR; A19339; A10339.
PDB; 1HPH; 10-JUL-95.
PDB; 1TH; 15-OCT-97.
PDB; 1ZWB; 12-MAR-97.
PDB; 1ZWB; 16-JUN-97.
PDB; 1ZWB; 16-JUN-97.
PDB; 1ZWB; 16-JUN-97.
PDB; 1ZWB; 16-JUN-97.
Query Match 100.0%; Plest Local Similarity 100.0%; Best Local Similarity Conservative Matches 8; Conservative
                                                   CONFLICT
SEQUENCE
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                                                                                       VARIANT
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                                                                                                                                          PS00335; PARATHYROID; 1.
SIGNAL; DISEASE MUTATION;
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12-MAR-97.
12-MAR-97.
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12861 MW;
                                                             PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEFFICIENT C PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
1; 243E87C7 CRC32;
            Score 54; DB 1; Let pred. No. 4.02e-03; 0; Mismatches 0;
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FORSSMANN W.-G.,
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PO1269;
21-JUL-1986 (REL. 01, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN)
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Best Local S
Matches
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MEDLINE; 87316938.
SCHMELZER H.-J., GRO
NUCLEIC ACIDS RES. 1
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
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SEQUENCE; 76018954.
MEDILINE; 76018954.
CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W., BIOCHEMISTRY 14:3631-3635(1975).
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SAUGR R.T., NIALL B.C.,
SAUGR R.T., I. J. J.,
POTTS J.T. J.R.,
BIOCHEMISTRY 13:1994-1999(1974).
BIOCHEMISTRY BELEVATES CALCIUM LEVEL BY DISSOLVING
1- FUNCTION: PTH ELEVATES CALCIUM LEXCRETION.
BONE AND PREVENTING THEIR RENAL EXCRETION.
TOS722; G1839; T.
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MEDLINE: 74253317.
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PIR; A01535; PTPG
PIR; B26806; B26806.
BBCKITE; PS00335; PARATHYROID;
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HORMONE; SIGNAL.
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S. 15:6740-6740(1987)
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12852 MW;
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Copyright (c) 1993-1998 University of Edinburgh, U
Distribution rights by Oxford Molecular Ltd
 protein - protein database search, using
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R58291
R49697
W20002
W20003
W17962
R74516
R74451
R74457
                                                                                                                                                                                                                                    R22072
R62432
R58079
R58081
R58049
               R58249
R58285
R58069
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                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues
              Modified [D-Trp_12,Ty Accelerator peptide b [LB,H10,Q18,R22,T33,A [LB,E10,Q18,R22,T33,A [LB,E10,Q18,R22,T33,A4]-[LB,C10,K11,Q16,D17,L [LB,Q16,R22,T33,A34]-[Lys(For)26,Lys(For)26,Lys(For)26,Cyclised rat parathyr Cyclised rat parathyr Cyclised [N1e 8,18,T Human pTH analogue [C Parathyroid hormone p [Ala16]-hpTH(1-36)-N [L1-Ser1]-hpTH(1-36)-N [Ala23]-hpTH(1-36)-N [Ala23]-hpTH(1-36)-N [Ala23]-hpTH(1-36)-N [L1-Ser1]-hpTH(1-36)-N [Ala23]-hpTH(1-36)-N [L1-Ser1]-hpTH(1-36)-N [L1-Ser1]-hpTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MasPar time 2.61 Seconds 52.810 Million cell updates/sec
N-alpha-methyl[Ala1]
                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scale 0.302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith-Waterman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research
                              1.66e+00
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							4																7	σ	9	_		
3	ALIGNMENTS	R23245	R21239	R21176	R21177	R21204	R21205	R21256	R23368	R21185	R23453	R23521	R23519	R23243	R23357	R23356	R23242	R23241	R23380	R21237	R23496	R21257	W25687	P30015	R58028	R58237	R58238	
		parathyroid hor 1.6	Human parathyroid hor 1.66e+00	parathyroid hor 1.6	1.6	1.6	e parathyroid h l.(	parathyroid ho 1.6	parathyroid ho 1.6	parathyroid hor 1.6	parathyroid ho 1.6	e parathyroid ho 1.6	parathyroid hor 1.6	parathyroid hor 1.6	e parathyroid ho 1.6	arathyroid hor 1.6	1.6	1.6	hor 1.6	oid hor 1.6	)-OH. 1.6	36) 1.6	-36)- 1.6					

#### claim 1; Column 10; 6pp; English. The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N.N-diisobutyl or 3-phenylpropancyl. The desamino form is also claimed. The PTH analogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bioactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bioassays to measure naturally occurring PTH and to diagnose the etiology of or to treat osteoporosis or hypercalcaemia. It may also be used to treat hyperthyroidism and diseases caused by abberrent prodn. of hormone-like substances, such as inflammation. It is prepd. by solid phase synthesis. See also R22058-75. Sequence osteoporosis and hyperparathyroidism. Claim 1; Column 10; 6pp; English. Key modified_site Synthetic. R22072 standard; Protein; 28 AA. R22072; 14-JUL-1992 (first entry) Modified [D-Trp_12,Tyr_34]rPTH(7-34)NH2. Parathyroid hormone; analogue; osteoporosis; hyperthyroidism; tumours; hypercalcaemia; renal failure; rat. New parathyroid hormone analogues - useful for treatment and vitro diagnosis of PTH-dependent tumours, immune disorders, WPI; 92-096233/12. (MERI ) MERCK & CO INC. Rosenblatt M, Roubini E, US5093233-A. 03-MAR-1992. modified_site 25-APR-1990; US-514394. 25-APR-1990; US-514394. AA; /note= "OTHER 28 Location/Qualifiers /label- NH2 'label= OTHER Chorev M, Nutt RF; ı see comments' in

Query Match Best Local S Matches

y Match 100.0%; Local Similarity 100.0%; hes 9; Conservative

Score Pred.

DB 4; L

Length 0

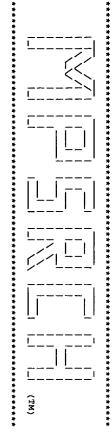
Mismatches N 68;

Indels

0

Gaps

0



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:14:22 1998; MasPar time 3.17 Seconds 103.833 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-32 (1-9) from US08817547A.pep 68 1 LRKKLQDVH 9

Scoring table:

PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 23.542; Variance 35.708; scale 0.659

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

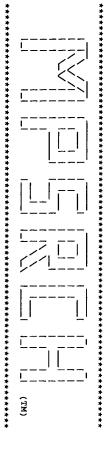
#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	O	v	4	ω	N	ь	sult No. s
54	ت 4-	54	54	54	54	54	54	58	68	88	83	83	83	83	83	83	83	68	83	68	68	68	score
	79.4	9	79.4	79.4	79.4	79.4	79.4	•	100.0	100.0	100.0			100.0		100.0	100.0	100.0	٠	٠		100.0	% Query Match
421	421	421	421	421	421	421	119	105	115	115	115	115	115	37	37	36	35	34	34	34	34	34	Length
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1SESB	1SESA	1SETB	1SETA	1SRYB	S38948	1SRYA	A34937	I51851	A05091	PTHU	JC4202	OHIG	PTPG	1ZWC	1HPH	1ZWB	1ZWD	1ZWA	12WE	1HTH	12WF	1ZWG	ID
-trna synthetas	l-trna synthetas	-trna	trna	Seryl-trna synthetase	serinetRNA ligase (	synthetas	parathyroid hormone p	hormone	hormone	parathyroid hormone p	parathyroid hormone -	hormone	parathyroid hormone p		parathyroid hormone f	parathyroid hormone (	parathyroid hormone (		roid	cyclic parathyroid ho	parathyroid hormone 4		Description
			6.51e+00	6.51e+00	6.51e+00	6.51e+00	6.51e+00	1.26e+00	1.61e-02		1.61e-02	- 1	.61e-		.61e-	1.61e-02	1.61e-02	1.61e-02	1.61e-02	e-0	1.61e-02		Pred. No.

45	44	43	42	41	40	39	3 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24
48	48	48	48	49	49	50	50	50	50	50	50	50	50	51	51	51	52	52	52	53	54
٠		70.6	70.6	72.1	72.1	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	75.0	75.0		•	76.5	•	•	79.4
1126	444	229	154	630	215	4725	1972	1938	621	586	569	437	412	1200	317	257	2475	879	878	348	421
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S04716	S09681	G70073	S03242	C64302	S35640	A44357	JC5420	JC5421	S10450	S44850	S62851	C64113	S07537	S77524	S45708	S53306	S35307	S22028	S20486	S45890	1SERB
DNA-directed RNA poly	citrate transport pro	two-component respons	hypothetical protein	hypothetical protein	hypothetical protein	dynein heavy chain, c	smooth muscle myosin	smooth muscle myosin	myosin heavy chain -	K12H4.1 protein - Cae	MG397 homolog D02_orf	tetrahydrofolylpolygl	myosin heavy chain, c	chromosome segregatio	MSH receptor - bovine	otic pı	polyprotein pp220 pre	paramyosin, standard	paramyosin - fruit fl	ODP1 protein - yeast	seryl-tRNA synthetase
6.64e+01	6.64e+01	6.64e+01	6.64e+01	4.57e+01	4.57e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	2.13e+01	2.13e+01	2.13e+01	1.44e+01	1.44e+01	1.44e+01	9.70e+00	6.51e+00

#book	REFERENCE	<pre>#submission submitted to #cross-references PDB:12WF</pre>	#authors	ORGANISM	ALTERNATE_NAMES PDB_TITLE	TITLE	RESULT 2	Qy 1 LRKKLQDVH	Db 21 LRKKLQDVH 29	Query Match Best Local Similarity Matches 9; Conse	2-9 15-25 SUMMARY	KEYWORDS FEATURE	COMMENT Resolu	#500X	#authors	REFERENCE	#Submission submitted to	#authors	REFERENCE	PDB_TITLE ORGANISM	ALTERNATE_NAMES	TITLE	RESULT 1
in Strukturen Verschiedener Parathormonfragmente in Loesung,	TN003318	the	J.C.	NMR, 10 structures #formal_name synthetic	<pre>n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone,</pre>	parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic	17ME #tvop complete	DVH 9	DVH 29	100.0%; Score 68; DB 5; Length 34; ilarity 100.0%; Pred. No. 1.61e-02; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	disease mutation; hormone; signal	Resolution: not applicable Determination: NMR	<pre>pp.0, Bayreuth : University of Bayreuth (Thesis), 1996</pre>	•	TN003319	submitted to the Brooknaven Protein Data Bank, June 1990 aces PDB:12WG	Marx, U.C.	A67743	<pre>succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic</pre>	ı	parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	

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COMMENT
COMMEN
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

: no n Thu Jul 30 11:13:17 1998; MasPar time 2.13 Seconds 105.752 Million cell updates/sec

abular output not generated.

Title: Description: Perfect Score: >US-08-817-547A-32 (1-9) from US08817547A.pep 68 1 LRKKLQDVH 9

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 24.742; Variance 29.653; scale 0.834

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

100.0 115 1 PTHY_BOVIN PARATHYROID 100.0 115 1 PTHY_CANFA PARATHYROID 100.0 115 1 PTHY_FIG 100.0 115 1 PTHY_FIG 100.0 115 1 PTHY_RAT PARATHYROID 100.0 115 1 PTHY_HUMAN PARATHYROID 100.0 115 1 PTHY_HUMAN PARATHYROID 79.4 119 1 PTHY_CHICK PARATHYROID 79.4 121 SYS_THETH SERYL-TRNA S 77.9 348 1 HWTL_YEAST HURNP ARGINI 76.5 621 1 YOKE_MYCTU HYPOTHETICAL	76.5 879 1 MYSP_DROME 75.0 310 1 SYNK_ARATH	73.5 569 1 X397_MYCPN 73.5 486 1 YM61_CAEEL 73.5 4725 1 DYHC_DICDI 72.1 209 1 VS10_ROTBS 72.1 630 1 Y019_METJA 70.6 129 1 YXDZ_BACSU 70.6 360 1 HISB_LACLA	.5 569 1 Y397_MYCPN .5 586 1 YM6L_CAEEL .5 4725 1 DYHC_DICDI .1 209 1 YS10_ROTBS .1 630 1 Y019_METJA .6 154 1 Y17K_SSV1 .6 229 1 YXDJ_BACSU .6 360 1 HISB_LACLA .6 419 1 PEXB_LACLA .6 419 1 CITI_KLEPN
75.0 310 1 SYNK_ARATH SYNTAXIN-REL		73.5 569 1 X397_MYCPN 73.5 4586 1 YM61_CAEEL 73.5 4725 1 DYHC_DICDI 72.1 209 1 VS10_ROTBS 72.1 630 1 Y019_METJA 70.6 136 1 Y17K_SSY1 70.6 229 1 YXDZ_BACSU 70.6 360 1 HISB_LACLA	73.5 569 1 Y397_MYCPN 73.5 4725 1 DYHC_DICD1 73.5 4725 1 DYHC_DICD1 72.1 209 1 VS10_ROTBS 72.1 630 1 Y1019_METUA 70.6 154 1 Y17K_SSV1 70.6 229 1 YXDJ_BACSU 70.6 310 1 HISB_LACIA 70.6 419 1 PEXA_PICPA 70.6 444 1 CITI_KLEPN
75.5 6/9 1 MISP_DROWNE 75.0 310 1 SYNK_ARATH 75.0 317 1 MSHR_BOVIN 73.5 437 1 FOLC.HAEIN	75.0 317 1 MSHR_BOVIN 73.5 437 1 FOLC_HAEIN	73.5 4725 1 DYHC_DICDI 72.1 209 1 VS10_ROTBS 72.1 630 1 V019_METJA 70.6 154 1 Y17K_SV1 70.6 229 1 YXDJ_BACSU 70.6 360 1 HIS8_LACLA	73.5 4725 1 DYHC_DICDI 73.5 4725 1 DYHC_DICDI 72.1 209 1 VSIO_ROTBS 72.1 630 1 Y1019_METJA 70.6 154 1 Y17K_SSV1 70.6 229 1 YXDJ_BACSU 70.6 320 1 HISB_LACLA 70.6 419 1 PEXA_PICPA 70.6 444 1 CITI_KLEPN
75.0 310 1 SYNK, ARATH 75.0 317 1 MSHR_BOVIN 75.0 317 1 FOLC_HAEIN 73.5 437 1 FOLC_HAEIN 73.5 650 1 Y397_MYCPN 73.5 560 1 Y461_GARTH	75.0 317 1 MSHR_BOVIN 73.5 437 1 FOLC_HAEIN 73.5 569 1 Y397_MYCPN 73.5 566 1 YM61 CAPET	72.1 209 1 VS10_ROTBS 72.1 630 1 Y019_METUA 70.6 154 1 Y17K_SSV1 70.6 229 1 YXDJ_BACSU 70.6 360 1 HIS8_LACLA	72.1 209 1 VS10_ROTBS 72.1 630 1 VO19_METJA 70.6 154 1 Y17K_SSV1 70.6 229 1 YXDJ_BACSU 70.6 360 1 HISB_LACLA 70.6 3419 1 PEXA_PICPA 70.6 444 1 CITI_KLEPN
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75.0 310 1 SYNK ARATH 75.0 317 1 MSHR_BOVIN 73.5 437 1 FOLC_HAEIN 73.5 586 1 YM61_CAEEL 73.5 4725 1 DYHC_DICDI 73.5 4725 1 DYHC_DICDI 73.1 209 1 VS10_ROTBS	75.0 317 1 MSHR_BOVIN 73.5 437 1 FOLC_HAEIN 73.5 569 1 Y397_MYCPN 73.5 4725 1 DYHG_DICDI 73.5 4725 1 DYHG_DICDI 72.1 209 1 VS10_ROTBS	70.6 229 1 YXDJ_BACSU 70.6 360 1 HIS8_LACLA	70.6 229 1 YXDJ BACSU 70.6 360 1 HIS LACLA 70.6 419 1 PEXA PICPA 70.6 444 1 CITI_KLEPN
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75.0 317 1 MINTELLINOME 75.0 317 1 MYHR_BOVIN 73.5 437 1 FOLC_HAEIN 73.5 437 1 FOLC_HAEIN 73.5 586 1 YMG_CAEEL 73.5 4725 1 DYHC_DICDI 73.5 4725 1 DYHC_DICDI 73.1 209 1 VSIO_ROTBS 72.1 209 1 VSIO_ROTBS 72.1 209 1 YIN_SSV1 70.6 154 1 YIN_BACSU	75.0 317 1 MSHR_BOVIN 73.5 437 1 FOLC_HAEIN 73.5 569 1 Y397_MYCPN 73.5 4725 1 DYHC_DICDI 73.5 4725 1 DYHC_DICDI 72.1 209 1 VS10_ROTBS 72.1 630 1 Y10_METUA 70.6 154 1 Y17K_SV1 70.6 229 1 YXDJ_BACSU		70.6 419 1 PEXA_PICPA 70.6 444 1 CIT1_KLEPN

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	47	47	48	48	48	48	48
67.6	67.6	67.6	•	•	67.6	•	•	67.6	67.6	67.6	67.6	67.6	67.6	67.6	69.1	•	70.6		•	70.6	70.6
2492	2492	1231	1036	793	754	745	637	590	509	457	447	380	326	184	112	100	1126	926	920	857	669
<b>ب</b>	سر	ب	ш	H	ب	_	ш	Н	ب	_	_	_	_	μ	۳	<u>, , , , , , , , , , , , , , , , , , , </u>	_	ш	Н	ب	H
POLN_EEVV3	POLN_EEVVT	KIF4_MOUSE	YAN2_SCHPO	KATA_ARATH	KATC_ARATH	KATB_ARATH	PTMA_ECOLI	YM63_YEAST	CPT7_PIG	EMB8_PICGL	KCC2_YEAST	CAPM_STAAU	YIE1_YEAST	GLG2_ARATH	YI91_SHIDY	YI91_ECOLI	RPOB_SULAC	PQQL_HAEIN	YML1_YEAST	MEDB_GIALA	YMS2_YEAST
NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	KINESIN-LIKE PROTEIN K	HYPOTHETICAL 117.4 KD	KINESIN-LIKE PROTEIN A	KINESIN-LIKE PROTEIN C	KINESIN-LIKE PROTEIN B	PTS SYSTEM, MANNITOL-S	HYPOTHETICAL 67.7 KD P	CYTOCHROME P450 XVIIA1	LATE EMBRYOGENESIS ABU	CALCIUM/CALMODULIN-DEP	CAPM PROTEIN.	36.7 KD PROTEIN IN CBR	GLUCOSE-1-PHOSPHATE AD	INSERTION ELEMENT IS91	INSERTION ELEMENT IS91	DNA-DIRECTED RNA POLYM	PROBABLE ZINC PROTEASE	HYPOTHETICAL 104.8 KD	MEDIAN BODY PROTEIN.	HYPOTHETICAL 76.2 KD P
4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	2.97e+01	2.97e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01

RRP	R R	R A	Z	RP ?	g P	RĀ	RA	꽃 주	Z	P.	₽3	장	RN	RL	RΑ	RX	ŖΡ	R i	RL	R 5	RP	RN	RL	RA A	RA.	7 7	RN	გ	റ്റ	တ္ထ	ი ლ	į	ğ	DT	Å	ij	RESULT
SEQUENCE OF 32-115. MEDLINE; 71063634.	S Z. PHYSIOL. C	AURBACH G.D., POTTS J.T. JR.;		SEQUENCE OF 32-115.	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).	D.V.;	_	MEDLINE: 74142666.	[0]		WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;	SEQUENCE FROM N.A.		NDOCRINOL. 28:411-424			SEQUENCE FROM N.A.		ACAD. SCI. U.S.A. 78:40	WEAVER C.A., GORDON D.F., KEMPER B.;			NATL. ACAD	JR., RICH A.:	של	SEQUENCE FROM N.A.		ARTIODACTYLA.	ARYOTA; METAZOA;	BOS TAURUS (BOVINE).	PTH.	(REL. 35, LAST ANNOTATION UPDAY	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	(REL. 01,	58;	PTHY BOVIN STANDARD; PRT; 115 AA.	TLT 1

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RESULT
AC PE
AC PE
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DT 01
DT 02
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CN P1
CN P2
CN CE CO
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                                                      Query Match
Best Local S
Matches
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A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,

A DEFTOS L.J., DAWSON B.F., HOGAN M.L., AMBACH G.D.;

AL DEFTOS L.J., DAWSON B.F., HOGAN M.L., AMBACH G.D.;

AL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

C BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; V00106; G85; -.

EMBL; J00024; G163641; -.

EMBL; J00024; G163643; -.

EMBL; J00024; E18250; ALT_INIT.

EMBL; J00024; E18250; ALT_INIT.

EMBL; M25082; G163645; -.

BEBL; K01938; G163645; -.

BEBL; M25082; G163645; -.

BEBL; M25082; G163645; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                           PROPEP
CHAIN
SEQUENCE
                                                                                                                                                          SEQUENCE FROM N.A.

TISSUE-PARATHYROID;

MEDLINE; 95369696.

ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

DEWILLE J.W., CAPEN C.C.;

GENE 160:241-243(1995).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS:

BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; U15662; G58916; ---

PROSITE; PS00335; PARATHYROID; 1.

HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HORMONE;
SIGNAL
PROPEP
CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                   CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                                                                  JT 2
PTHY_CANFA STANDARD; PRT; 115 AA.
P52212;
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BREWER H.B. JR., RONAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
                    55 LRKKLQDVH 63
 μ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 LRKKLQDVH 63
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LRKKLQDVH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A24949; A24949.
                                                   h 100.0%;
Similarity 100.0%;
9; Conservative
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1 25

26 31

26 31

15 32 115

17 106 106

V

18 115 AA; 12980 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00335; PARATHYROID; 1.
                                                                                                         1
26
32
115 AA;
                                                                                                         25
31
115
12957
                                                                                                           MW;
                                                   Score 68; DB 1; L
Pred. No. 8.13e-04;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 1; Length 115; Pred. No. 8.13e-04; 0; Mismatches 0; Indels
                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                         16ED0EBC CRC32;
                                                                            Length 115;
                                                   0
                                                  Indels
                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                  Gaps
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                                                  0
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Search completed: Thu Jul 30 11:13:23 1998 Job time: 6 secs.

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Description:
Perfect Score:
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                                                                                                                                                                                                                                                                                                                                                    Post-processing:
                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPsrch_pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                         abular output not generated
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    100
110
112
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118
                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
    protein - protein database search, using Smith-Waterman algorithm
                                                                                                                                                                                        Query
Match
    PAM 150
Gap 15
                                                                                                                                                                                                                                                                                                                                                                                                                      >US-08-817-547A-32
(1-9) from US08817547A.pep
68
                                                                                                                                                                                                                                                                                     sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified
                                                                                                                                                                                                                                                                                                                                          Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                      Mean 23.769; Variance 29.317; scale 0.811
                                                                                                                                                                                                                                                                                                                                                                    140542 seqs, 42109429 residues
                                                                                                                                                                                                                                                                                                                                                                                                                1 LRKKLQDVH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thu Jul 30 11:13:41 1998;
    Length DB
   10
3
3
3
11
11
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10
                   Q1757
Q17757
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Q17757
Q1787
Q17757
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Q17334
Q17970
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TARTAN PROTEIN PRECURS CHROMOSOME SEGREGATION MYOSIN HEAVY CHAIN (AA C14C10.1. MYOSIN HEAVY CHAIN 21 MYOSIN. MYOSIN. MYOSIN. MYOSIN. MYOSIN LIGHT CHAIN KIN MYOSIN LIGHT CHAIN KIN
                                                                                                        C06G3.9 PROTEIN.
SIMILAR TO SACCHAROMYC
PUTATIVE N6-ADEININE S
RAD50.
POLYPROTEIN PP220.
MADS-BOX FAMILY TRANSC
PUTATIVE MADS-BOX FAMILY
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                                                                                BOX PROTEIN.
MELANOCYTE STIMULATING
MC1-R PROTEIN.
                                                                                                                                                                     PARATHYROID HORMONE
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2.54e+00
4.08e+00
4.08e+00
6.52e+00
6.52e+00
6.52e+00
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1.04e+01
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RESULT ID Q11 AC Q17 DT 01 DT 01 DT 01 DT C00 GN CO6 GN CO6 GN CA6 OC EUF RN SEC RC STI RA SUL	Query I Best La Matche Db 4!	IRESULT  OF ACT	44444333333333222222222222222222222222
LT 2 Q17750; PRELIMINARY; P Q17750; O1-NOV-1996 (TREMBLREL. 01, CRE 01-NOV-1996 (TREMBLREL. 05, LAS 01-JAN-1998 (TREMBLREL. 05, LAS (C16G3.9 PROTEIN. C16G3.9 P	Match 85.3%; scal Similarity 88.9%; s 8; Conservative 5 LRKKLQDGH 53	Q63473 Q63473 Q63473; Q63473; Q1-NOV-1996 (TREMBLREL 01, CRI 01-NOV-1996 (TREMBLREL 05, LAX Q1-JAN 1998 (TREMBLREL 05, LAX Q1-JAN 1998 (TREMBLREL) Q5, LAX Q1-JAN 1998 (TREMBLREL) Q6, LAX Q1-JAN 1998 (TREMBLREL) Q7H. RATTUS NORVEGICUS (RAT). EUTHARYOTA; METAZOA; CHORDATA; \Q1 EUTHERIA; RODENTIA. [1] SEQUENCE FROM N.A. TISSUE-THYROID, AND PARATHYROII SCHMELER H.J., GROSS G., MAYEJ ADV. GENE TECHNUL, 21:28-229( EMBL; M54875; G601933; NON_TER 10 1 1 1	49 72.1 1914 2 0.1 48 70.6 360 9 0.3 48 70.6 481 3 0.4 48 70.6 1583 2 0.4 48 70.6 1583 2 0.4 48 70.6 2346 3 0.4 48 70.6 2346 3 0.4 47 69.1 485 3 0.4 47 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 862 10 0.4 69.1 2708 3 0.4 69.1 2708 3 0.4 69.1 2708 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2819 3 0.4 69.1 2
RT; 7 ATED) T SEQUE T ANNOT ; NEMAT	Score 58; Pred. No. 0; Misma	PRT; 1 EATED) ST SEQUE ST ANNOT	Q15746 Q15746 Q15746 Q000321 Q000328 Q18255 Q18255 Q15045 Q15045 Q15045 Q15045 Q15045 Q15045 Q15045 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873 Q16873
35 AA.  NCE UPDATE) ATION UPDATE)  ODA; SECERNENTEA; RHABDITIDA  DBJ DATA BANKS.	DB 10; Length 105; 2.16e-01; tches 1; Indels 0; C	05 AA. NCE UPDATE) ATION UPDATE) TA; TETRAPODA; MAMMALIA;	MYOSIN LIGHT CHAIN KIN POLYPEPTIDE DEFORMYLAS 2 HISC. C38C3.3 PROTEIN. C28C3.3 PROTEIN. C18C3.3 PROTEIN INTERACTING COSMID C2709. HUNTINGTIN INTERACTING SIMILARITY TO MYOSIN H KIAA0336.  TPR HOMOLOG. CONSERVED HYDOTHETICAL FISSION YEAST (FRAGMEN 2 ARA70. ORF695. CHICKEN RABAPTIN-5. RAT RABAPTIN-5. RAT RABAPTIN-5. RAT RABAPTIN-5. RAT RABAPTIN-5. CHICRONQUINE RESISTANCE CHLOROQUINE RESISTANCE CHLOROQUINE RESISTANCE STRAIN HB3 CG2 (CG2).
ſDA.	Gaps 0.		1.64e+01 2.56e+01 2.56e+01 2.56e+01 2.56e+01 2.56e+01 2.56e+01 2.56e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01 3.99e+01

DR EMBL: U61947; G1397274; ..., 2002 Marches 735 AA: 81001 NM; 84A565C0 CRC32; 2002 Match 735 AA: 81001 NM; 84A565C0 CRC32; 2002 Matches 6; 79.4%; Score 54; DB 3; Length 735; 2002 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0; 2002 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0; 2002 Matches 0; Indels 0; 2002 Matches 0; Indels 0; 2002 Matches 0; Indels 0; 2002 Matches 0; 2002

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:17:36 1998; MasPar time 2.58 Seconds 47.571 Million cell upda

updates/sec

Description: Perfect Score: Title: abular output not generated (1-8) from US08817547A.pep 59 1 LRKKLQDV 8 >US-08-817-547A-33

Scoring table: PAM 150 Gap 15 Sequence:

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.574; Variance 53.366; scale 0.311

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 2 3 3 3 4 4 4 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	esult No.
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	Score
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Q C C C C C C C C C C C C C C C C C C C	Length
2 2 2 2 2 2 4 4 4 9 9 9 9 9 9 9 9 9 9 9	BG
R580432 R580433 R580483 R580079 R580079 R58291 R749697 R74486 R744485 R744485 R744485 R744885 R758191 R58253 R58253	ID
Modified [D-Trp_12,Ty Accelerator peptide b [LB,Q10,Q18,R22,T33,A34]-[LB,Q16,R22,T33,A34]-[LB,G16,R22,T33,A34]-[LB,G10,Q18,R22,T33,A]-[LYS,For)26, LyS,For)26, LyS	Description
9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.	Pred. No.

100.0 38 9 R58022 [11el]-hrm(1-30) 100.0 38 9 R58023 [11el]-hrm(1-30) 100.0 44 26 P30015 Human parathyroid hor 100.0 84 27 W25687 Human parathyroid hor 100.0 84 4 R23246 Human parathyroid hor 100.0 84 4 R23241 Human parathyroid hor 100.0 84 4 R23342 Human parathyroid hor 100.0 84 4 R23356 Bovine parathyroid hor 100.0 84 4 R23357 Bovine parathyroid hor 100.0 84 4 R23357 Human parathyroid hor 100.0 84 4 R23357 Human parathyroid hor 100.0 84 4 R23357 Human parathyroid hor 100.0 84 4 R23243 Human parathyroid hor 100.0 84 4 R23243 Human parathyroid hor 100.0 84 4 R23251 Bovine parathyroid hor 100.0 84 4 R23519 Bovine parathyroid hor 100.0 84 4 R23521 Bovine parathyroid hor 100.0 84 4 R23185 Bovine parathyroid hor 100.0 84 4 R23185 Bovine parathyroid hor 100.0 84 4 R23185 Bovine parathyroid hor 100.0 84 4 R23186 Bovine parathyroid hor 100.0 84 4 R23264 Human parathyroid hor 100.0 84 4 R23266 Human parathyroid hor 100.0 84 4 R23266 Human parathyroid hor 100.0 84 4 R23267 Bovine parathyroid hor 100.0 84 4 R23176 Human parathyroid hor 100.0 84 4 R23176 Human parathyroid hor 100.0 84 4 R23245 Human parathyroid hor 100.
3 9 R58022 [Ile1]-hPTH (1
9 K58023 [INMERINE 34] "ILE 17] "HOTH (1 6) 9 K58023 [Ala1, Abu2 or 9 F58023 [Ala1, Abu2 or 9 F5802] Human parath) 4 K23343 Human parath) 4 K23453 Human parath) 4 K23521 Bovine parath 4 K23521 Bovine parath 4 K23453 Human parath) 4 K2356 Human parath) 4 K2356 Human parath) 4 K21176 Human p
9 R58023 [INMERINE 34] "INFORMATION OF R58023 [Alal, Abu2 or 9 R5802] [Alal, Abu2 or 9 R5802 [Alal, Abu2 or 9 R5802] [Alal, Abu2 or 9 R5802 [Alal, Abu2 or 9 R5802] [Alal, Abu
[Iled]-hpfH[[Iled]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[] [Iled]-hpfH[]-hpfH[] [Iled]-hpfH[]-hpfH[] [Iled]-hpfH[]-hpfH[] [Iled]-hpfH[]-hpfH[]-hpfH[] [Iled]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfH[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM[]-hpfHM
rathy

# R22072; R22072 standard; Protein; 28 AA.

ALIGNMENTS

14-JUL-1992 (first entry)
Modified [0-Trp_12,Tyr_34]rPTH(7-34)NH2.
Parathyroid hormone; analogue; osteoporosis; hyperthyroidism; tumours; hypercalcaemia; renal failure; rat.
Synthetic. modified_site modified_site /label= OTHER /note= "OTHER • 28 /label= NH2 Location/Qualifiers . see comments'

03-MAR-1992. 03-MAR-1990: 514394. 25-APR-1990: US-514394. 25-APR-1990: US-514394. (MERI ) MERCK & CO INC. ROSenblatt M, Roubini E, Chorev M, Nutt RF; WPI; 92-096233/12. US5093233-A.

PT New parathyroid hormone analogues - useful for treatment and in PT vitro diagnosis of PTH-dependent tumours, immune disorders, PT osteoporosis and hyperparathyroidism.

CC claim 1; Column 10; 6pp; English.

PS Claim 1; Column 10; 6pp; English.

CC amino acid gp. by N.N-diisobutyl or 3-phenylpropanoyl. The peptide is modified at Lysl3 (of the parent PTH) in the epsilon affinity to the peptide hormone receptor without activating the 2nd caffinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the CC bloactive conformation of PTH to enhance the activity. The peptide CC may be used in in vitro bioassays to measure naturally occurring CTH and to diagnose the etiology of or to treat osteoporosis or hypercalcaemia. It may also be used to treat hyperthyroidism and C diseases caused by abberrent prodn. of hormone-like substances, Such as tumours. It may also be used to treat immune diseases such as inflammation. It is prepd. by solid phase synthesis. Sequence 28 AA;

Query Match Best Local ( Matches y Match 100.0%; Local Similarity 100.0%; hes 8; Conservative Score 59; DB 4; Ler Pred. No. 9.92e+00; 0; Mismatches 0; Length 28; Indels 0 Gaps 0

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18 lrkklqdv 25 ||||||| 1 LRKKLQDV 8

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                                                                                                                                                                                                                                                                                                                                                                                          PP 13-AUG-1994.

PP 13-AUG-1994.

PP 10-FEB-1993; 045998.

PP 10-FEB-1993; 19-045998.

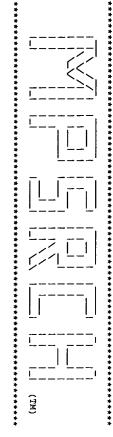
RCGELERATOR CHEM IND CO LTD.

WPI; 95-157631/21.

Accelerator for regenerating periodontal tissue - comprises Accelerator for regenerating periodontal tissue - comprises Accelerator for regenerating periodontal tissue - comprises Accelerator in Accelerator aminoacid residues

PT aminoacid residues

The accelerator accelerator may be used to calso comprises a cell growth factor. The accelerator may be used to cacelerate the growth of periodontal tissue regeneration. The accelerator is applied by opening the ginglva, treating the tissue capting by periodontal pocket. The accelerator reduces the down growth of the capting the accelerator in the ca
                                                                                                                                                                                                용
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Best Local Similarity 100.0%;
Matches 8; Conservative
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R62432;
R62432;
31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva; periodontal tissue; regeneration; periodontaltis; periodontal tocket; down growth; epithelium; fibre adhesion; cement.
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                                                                                                                                        LRKKLQDV 8
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Pred. No. 9.92e+00;
0; Mismatches 0;
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Psrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 11:16:07 1998; MasPar time 3.11 Seconds 93.824 Million cell updates/sec

labular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-33 (1-8) from US08817547A.pep 59 1 LRKKLQDV 8

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 22.968; Variance 34.253; scale 0.671

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	DB
12WG 11WF 11WH 12WE 12WA 12WA 12WB 11HPH 12WB 11HPH 12WB 11HPH 12WB 11HPH 12WB 11HPH 12WB 11HPH 12WB 12WB 13WB 13WB 13WB 13WB 13WB 13WB 13WB 13	Ħ
parathyroid hormone 4 cyclic parathyroid hormone 4 cyclic parathyroid hormone ( parathyroid hormone p parathyroid hormone c polyprotein pp220 pre floral homeotic prote floral homeotic prote floral hormone right serine -tRNA ligase ( seril-trna synthetase Seryl-trna synthetase Seryl-trna synthetase	0
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79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	81.4	81.4	83.1	83.1	84.7	84.7	84.7	84.7	84.7	84.7	84.7	84.7	84.7	
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myosin heavy chain, n	∍gregati	RET oncogene fusion p	DNA primase homolog -	conserved hypothetica	hypothetical protein	hypothetical protein	hypothetical 11.6K pr	DNA-directed RNA poly	hypothetical protein		hypothetical protein	dynein heavy chain, c	smooth muscle myosin	smooth muscle myosin	myosin heavy chain -	K12H4.1 protein - Cae	tetrahydrofolylpolygl	L-trna	Seryl-trna synthetase	Seryl-trna synthetase	Condition of the condition of
6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01		6.49e+01		4.43e+01	4.43e+01	3.01e+01	3.01e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01	2 . 000

ORGANISM REFERENCE #authors #submission #cross-refere REFERENCE #authors #book	SULT TRY TLE	Query Match Best Local Simil Matches 8; Matches 21 LRKKLODV Db 21 LRKKLODV Qy 1 LRKKLODV	COMMENT Resol COMMENT Deter KEYWORDS FEATURE 2-9 15-25 SUMMARY	miss miss-r CE hors	RESULT 1 ENTRY TITLE TITLE ALTERNATE_NAMES POB_TITLE ORGANISM REFERENCE
TITLE Structure of n-terminal acetylated human parathyroid normone,  NMR, 10 structures  ANISM #formal_name synthetic  ERENCE A67742  #authors Rosech, P: Marx, U.C.  #cross-references PDB:12WF  ERENCE TN003318  #authors Marx, U.C.  #authors in Strukturen Verschiedener Parathormonfragmente in Loesung,	ZWF #type complete arathyroid hormone 4 37 mutant N-TERMINAL ACETYLATER synthetic -acetyl-hpth(4-37)	100.0 arity 100.0 Conservativ 28	Resolution: not applicable  Determination: NMR disease mutation; hormone; signal  #region helix (right hand alpha)\ #region helix (right hand alpha)  #length 34 #molecular-weight 4128 #checksum 5508	#authors Roesch, P.; Marx, U.C. #submission submitted to the Brookhaven Protein Data Bank, June 1996 #cross-references PDB:12WG ERENCE TN003319 #authors Marx, U.C. #authors Marx, U.C. #authors in Strukturen Verschiedener Parathormonfragmente in Loesung, #book in Strukturen Verschiedener Parathormonfragmente in Loesung, #book pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic n-succinyl-hpth(4-37) succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic A67743

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COMMENT Resolution: not applicable
COMMENT REMAINS.

COMMENT REMAINS.

COMMENT REMAINS.

REMAINSE Details.

14-27 SUMMARY # #region helix (right hand alpha) |

14-27 # #length 34 #molecular-weight 4128 #checksum 5508

SUMMARY # #length 34 #molecular-weight 4128 #checksum 5508

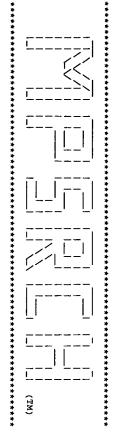
Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 LERKLODV 8

Search completed: Thu Jul 30 11:16:30 1998

search completed: Thu Jul 30 11:16:30 1998
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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:15:44 1998; MasPar time 2.11 Seconds 95.235 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-33 (1-8) from US08817547A.pep 59

1 LRKKLQDV 8

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 24.101; Variance 28.427; scale 0.848

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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100.0 100.0 100.0 100.0 100.0 86.4 84.7 84.7 84.7 84.7 84.7 84.7 79.7 79.7 79.7 78.0	Query Match
115 115 115 115 115 115 110 310 310 317 437 437 4725 686 647 4725 100 110 110 110 110 1110 1110 1110 11	Length
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PTHY_BOVIN PTHY_CANFA PTHY_PIG PTHY_PIG PTHY_HUMAN SYNK_ARATH MSHR_BOVIN SYS_THETH FOLC_HAEIN YM61_CAEEL Y04E_MCTU DYHC_DICDI DYHC_DICDI DYHC_DICDI DYHC_DICDA Y17K_SSYJ PEXA_PICPA RPOB_SULAC Y191_ECULA Y17L_SHIDY RR14_PORPU TCTD_SALTY YXDD_BACSU Y1E1_YEAST	Ħ
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4.95e-02 4.95e-02 4.95e-02 4.95e-02 4.95e-02 2.83e+00 4.56e+00 4.56e+00 4.56e+00 4.56e+00 4.56e+00 4.56e+00 1.16e+01 1.16e+01 1.16e+01 1.83e+01 1.83e+01 2.86e+01 2.86e+01 2.86e+01 2.86e+01	Pred. No.

44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
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76.3 76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	78.0	78.0	78.0	78.0	78.0	78.0	78.0	•	•	78.0	•	78.0	78.0
834 1978	565	554	430	430	428	314	119	2492	2492	2492	2161	1231	857	806	793	754	745	637	509	447
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MYSG_CHICK	NO56_SOYBN	YER2_YEAST	GFAP_RAT	GFAP_MOUSE	GFAP_BOVIN	GCR_SHEEP	PTHY_CHICK	POLN_EEVV3	POLN_EEVVP	POLN_EEVVT	RRPL_CDVO	KIF4_MOUSE	MEDB_GIALA	SYFB_MYCGE	KATA_ARATH	KATC_ARATH	KATB_ARATH	PTMA_ECOLI	CPT7_PIG	KCC2_YEAST
SCD1 PROTEIN. MYOSIN HEAVY CHAIN, GI		HYPOTHETICAL 62.3 KD P	GLIAL FIBRILLARY ACIDI	GLIAL FIBRILLARY ACIDI	GLIAL FIBRILLARY ACIDI	GLUCOCORTICOID RECEPTO	PARATHYROID HORMONE PR	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	RNA POLYMERASE BETA SU	KINESIN-LIKE PROTEIN K	MEDIAN BODY PROTEIN.	PHENYLALANYL-TRNA SYNT	KINESIN-LIKE PROTEIN A	KINESIN-LIKE PROTEIN C	KINESIN-LIKE PROTEIN B	PTS SYSTEM, MANNITOL-S	CYTOCHROME P450 XVIIA1	CALCIUM/CALMODULIN-DEP
4.44e+01 4.44e+01	4.44e+01	4.44e+01	4.44e+01	4.44e+01	4.44e+01	4.44e+01	4.44e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	

R R	유	RA S	R	RP	Z Z	RA	RA :	R P	RN	₽ ₹	RX	RP	2 2	₽ &	RX	ŖΡ	RN	RĽ	R X	RP	RN	R.	2 3	0 X	RP	RN	8	88	) (C	D	ŊΤ	ij	ij	A l	RESULT
SEQUENCE OF 32-115. MEDLINE; 71063634.		AURBACH G.D., POTTS J.T. JR.;	O76162.	SEQUENCE OF 32-115.	PROC. NATE. ACAD. SCI. U.S.A. /1:653-656(19/4).	D.V.;		MEDITURE 74142666	•	GENE 28:319-329(1984).	62483.	SEQUENCE FROM N.A.		R C.A., GORDON D.F	MEDLINE; 83105964.	UENCE		ACAD. SCI. U.S.A. 78	WEAVER C.A., GORDON D.F., KEMPER B.;	SEQUENCE FROM N.A.		NATL ACAD. SCI.	TR BICH A:	B F MATZOIR T A NATHANG T SHARP D			ARTIODACTYLA.	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:		THYROID HORMONE PR	(REL. 35, LAST ANNOTATION UPDAY	1986 (REL. 01,	1986 (REL.	8	DTHY BOYTN STANDARD: PRT: 115 AA.

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Best Local Similarity 100.0%;
Matches 8; Conservative
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PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
[8]
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PIR; /
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P52212;
01-OCT-1996
01-OCT-1996
01-OCT-1996
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PROPEP
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MEDLINE; 95369696.

ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

DEWILLE J.W., CAPEN C.C.;

GENE 160:241-243(1995).

GENE 160:241-243(1995).

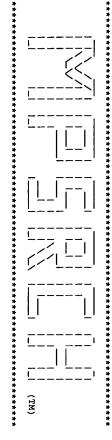
-1- FUNCTION: FYH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS

BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; U15662; G558916; -.

EMBL; U15662; G558916; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                        SIGNAL
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CHAIN
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Local Similarity 100.0%;
nes 8; Conservative
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A24949; A24949.
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   LRKKLODV 8
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32
115 AA;
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31
115 P
106 V
; 12980 MW;
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31 B)
115 P)
115 PW;
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V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                      Score 59; DB 1; Length 115;
Pred. No. 4.95e-02;
0; Mismatches 0; Indels
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BY SIMILARITY.
PARATHYROID HORMONE.
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                                                                                                                                                                 0,
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Search completed: Thu Jul 30 11:15:51 1998 Job time : 7 secs.



MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:16:49 1998; MasPar time 3.69 Seconds 91.339 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-817-547A-33 (1-8) from US08817547A.pep 59 1 LRKKLQDV 8

Title:

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 23.168; Variance 27.952; scale 0.829

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1 2 3 3 4 4 4 4 4 4 7 7 7 7 8 8 9 9 9 11 11 11 11 11 11 11 11 11 11 11	Result No.
44444555555555555555555555555555555555	Score
89.8 88.1 88.1 88.1 86.4 86.4 86.4 86.4 84.7 84.7 84.7 84.7 84.7 84.7 84.7 84	Query Match
398 929 929 2475 2475 242 257 3317 3317 3317 3317 3317 3317 317 317	Length
100 110 110 110 110 110 110 110 110 110	B
004471 0034473 0324473 0324970 040700 040700 040700 07037 010337 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333 010333	ID
SIMILAR TO SACCHAROMYC PARATHEROID HORMONE (F PUTATIVE NG-ADEININE S POLYPROTEIN PP220. PUTATIVE MADS-BOX FAMILY TRANSC BOX PROTEIN. MADS-BOX FAMILY TRANSC MELANCCYTE STIMULATING MC1-R PROTEIN. MYOSIN HEAVY CHAIN (AA MYOSIN HEAVY CHAIN 21 C06G3.9 PROTEIN. MYOSIN. POLYPEPTIDE DEFORMYLAS C38C3.3 PROTEIN. COSMID C27D9. TPR HOMOLOG. TPR HOMOLOG.	Description
1.35e+00 2.21e+00 2.21e+00 3.61e+00 3.61e+00 3.61e+00 3.61e+00 3.61e+00 5.84e+00 5.84e+00 5.84e+00 5.84e+00 5.84e+01 1.50e+01 1.50e+01 1.50e+01 1.50e+01 1.50e+01	Pred. No.

4.4	<u>.</u> (	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
46	2 6	4	46	46	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47
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2497	3 1	2493	1707	334	2819	2742	2708	2510	1999	1200	862	862	862	862	860	836	614	614	434	360	245	199	134	133
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Q88978	00000	066594	90896Q	Q17970	015792	015801	015791	Q94658	Q63731	P73340	Q15276	035551	P70609	035550	042351	263618	Q15307	Q13772	P78918	029516	Q40969	027967	P75679	P73917
NONSTRUCTURAL POLYPROT		NONSTRUCTURAL POLYPROT	PUTATIVE REPLICASE.	C14C10.1.	STRAIN HB3 CG2 (CG2).	CHLOROQUINE RESISTANCE	CHLOROQUINE RESISTANCE	EXPORTED SERINE/THREON	NEURONAL MYOSIN HEAVY	CHROMOSOME SEGREGATION	RABAPTIN-5.	MOUSE RABAPTIN-5.	RABAPTIN.	RAT RABAPTIN-5.	CHICKEN RABAPTIN-5.	ESPIN.	RET FUSED GENE.	ARA70.	FISSION YEAST (FRAGMEN	DNA PRIMASE, PUTATIVE.	PUTATIVE MADS-BOX FAMI	CONSERVED HYPOTHETICAL	FROM BASES 263572 TO 2	ä
3.75e+01			3.75e+01	3.75e+01	2.38e+01	2.38e+01	2.38e+01	•	٠	2.38e+01	2.38e+01	2.38e+01		2.38e+01	2.38e+01	2.38e+01		2.38e+01	2.38e+01		2.38e+01		2.38e+01	2.38e+0:

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SEQUENCE FROM N.A.		EUNARIOTA; METAZOA; CHORDATA; VERIEBRATA; TELRAFODA; MAMMALIA; EUTHERIA; RODENTIA.	RAT).	PTH.	HORMONE (FRAGMENT).	TREMBIRET OS LAST ANNOTATIO	01	(TREMBLREL		Q534/3 PRELIMINARY; PRT; LOS AA.	2	1 LRKKLQDV 8	= ;	328 LRKRLQEI 335	Matches 5; Conservative 3; Mismatches 0; indexs 0; Gaps 0;	cal Similarity 62.5%; Pred. No. 1.35e+00;	y Match 89.8%; Score 53;	OPO CATA TOOLS THE ACTION AND	SECTION 308 AA: 45530 MW. ODESOELE CRO32:	4.	D EMBL/GENBANK/DDBJ	N.A., THEOLOGIS A.;	IM C., KURTZ D., LI	ONWAY A.B., CON	ISKAIA V.S., OSBORNE B.I., TORIUMI M., YU G.,	STRAIN-CV. COLUMBIA;	SEQUENCE FROM N.A.	[1]	CAPPARALES; CRUCIFERAE.	PLANTA; EMBRYOPHYTA;	ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).	F5114.7.	SIMILAR TO SACCHAROMYCES HYPOTHETICAL PROTEIN P9642.2.	(TREMBLREL. 04, LAST ANNOTATION)	(TREMBLREL. 04,	01-JUL-1997 (TREMBLREL. 04, CREATED)	004471;	O04471 PRELIMINARY; PRT; 398 AA.	LT 1

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RC TISSUE-THYROLD, AMD PARATHYROLD;
RA SCHMELZER 1.3., GROSS G., MAYER H.;
LADY. GENE TECHNOL. 21:238-229(1984).

DEBLE MA4875, GROSS G., MAYER H.;
DN EMBLE MA4875, GROSS G., MAYER H.;
PRINCE 105 AA; 11746 MW; 6AC3163E CRC32;

OUNCY MATCh

Best Local Similarity 100:0%; Pred. No. 2:212+00;
MATChes 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

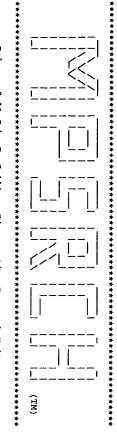
Db 45 LRKKLOD 51

Oy 1 LRKKLOD 51

Oy 1 LRKKLOD 7

Search completed: Thu Jul 30 11:17:18 1998

Job time: 29 secs.
```



MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:20:11 1998; MasPar time 2.56 Seconds 41.969 Million cell updates/sec

**Tabular output not generated** 

Title:

Description: Perfect Score: (1-7) from US08817547A.pep 52 1 LRKKLQD 7 >US-08-817-547A-34

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.842; Variance 50.654; scale 0.313

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

11111111111111111111111111111111111111	Result
55555555555555555555555555555555555555	Sco
	- G7
334 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 5
2 R03300 9 R58291 7 R34358 2 W200009 2 W200009 2 W17963 2 W17963 2 W17963 2 W17963 2 W17963 2 W17963 2 W17963 2 W17963 9 R74440 4 R74440 4 R74440 9 R58251 9 R582351 9 R582336	:
Human parathyroid hor [Lys(For) 26, Lys(For) 27, Lys(For) [Lys(For) 27, Lys(For) [Lys(For) 28, Lys(For) 28, Lys(For) 24, Lys(For) [Lys(2)] - hprid(1-34) - hprid(1-36) - h	Description
. 42444 E8446	
	1
3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01	Pred. No
	1 5

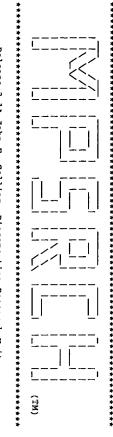
52 100.0 36 9 R58069   Isopropyl-[LB,KISopropyl-] 52 100.0 36 9 R58227   [D-Gln29]-hPTH(1-36)-52 100.0 38 9 R58136   [Arg14]-hPTH(1-38)-OH 52 100.0 38 9 R58108   [Arg14]-hPTH(1-38)-OH 52 100.0 84 42 R23356   Bovine parathyroid hor 52 100.0 84 4 R23357   Bovine parathyroid hor 52 100.0 84 4 R23357   Bovine parathyroid hor 52 100.0 84 4 R233242   Human parathyroid hor 52 100.0 84 4 R233242   Human parathyroid hor 52 100.0 84 4 R233243   Human parathyroid hor 52 100.0 84 4 R23521   Bovine parathyroid hor 52 100.0 84 4 R23243   Human parathyroid hor 52 100.0 84 4 R23243   Human parathyroid hor 52 100.0 84 4 R23243   Human parathyroid hor 52 100.0 84 4 R23243   Bovine parathyroid hor 52 100.0 84 4 R23273   Bovine parathyroid hor 52 100.0 84 4 R23273   Bovine parathyroid hor 52 100.0 84 4 R23256   Bovine parathyroid hor 52 100.0 84 4 R23256   Bovine parathyroid hor 52 100.0 84 4 R23257   Human parathyroid hor 52 100.0 84 4 R23258   Bovine parathyroid hor 52 100.0 84 4 R23259   Human parathyroid hor 53 100.0 84 4 R23259   Human parathyroid hor 54 100.0 84 4 R23259   Human parathyroid hor 55 100.0 84 4 R23259   Human parathyroid hor 56 100.0 84 4 R23259   Human parathyroid hor 57 100.0 84 4 R23259   Human parathyroid hor 58 100.0 84 4 R23259   Human parathyroid hor 59 100.0 84 4 R23259   Human parathyroid hor 50 100.0 84 4 R23259   Human parathyroid hor 50 100.0 84 4 R23259   Human parathyroid hor 51 100.0 84 4 R23259   Human parathyroid hor 52 100.0 84 4 R23259   Human parathyroid hor 53 100.0 84 4 R23259   Human parathyroid hor	45	44	43	42	41	40	39	38	37	36	ü	34	ယ	32	<u>3</u>	30	29	28	27	26	25	24	23	22	21	
36 9 R58069   Isopropy!-[LB.K(I of State of Stat																										
6 9 R58069 ISOPROPYI-[LB.KII 6 9 R5827 [D-Gln29]-hpTH(1-38 8 9 R58136 [Arg14]-hpTH(1-38 8 9 R58108 [Arg14]-hpTH(1-38 8 9 R58108 [Arg14]-hpTH(1-38 8 9 R58108 [Arg14]-hpTH(1-38 8 9 R58108 Human parathyroid 4 R23356 Bovine parathyroid 4 R23357 Bovine parathyroid 4 R23347 Human parathyroid 4 R23242 Human parathyroid 4 R23521 Bovine parathyroid 4 R23243 Human parathyroid 4 R23253 Bovine parathyroid 4 R23273 Human parathyroid 4 R23273 Bovine parathyroid 4 R23273 Human parathyroid 4 R23273 Bovine parathyroid 4 R23273 Bovine parathyroid 4 R23273 Bovine parathyroid 4 R23547 Bovine parathyroid 4 R23547 Bovine parathyroid 4 R23248 Human parathyroid 4 R23248 Human parathyroid 4 R23248 Human parathyroid	٠	٠	•	٠	٠	•	•	٠	٠	٠	٠			•					٠	٠	٠	٠	٠	•	8	0
9 R58069 ISOPTOPY1-[LB.K(I) 9 R58027 [D-Gln29]-hPTH(1-38 8 R58136 [Arg19]-hPTH(1-38 9 R58136 [Arg14]-hPTH(1-38 9 R58108 [Arg14]-hPTH(1-38 10 R2357 Human parathyroid 4 R23357 Bovine parathyroid 4 R23341 Human parathyroid 4 R23242 Human parathyroid 4 R23521 Porcine parathyroid 4 R23519 Bovine parathyroid 4 R23519 Bovine parathyroid 4 R23273 Bovine parathyroid 4 R23273 Bovine parathyroid 4 R23256 Human parathyroid 4 R23256 Bovine parathyroid 5 R23257 Human parathyroid 6 R23258 Bovine parathyroid 7 R23239 Human parathyroid 7 R23239 Human parathyroid 8 R23239 Human parathyroid 8 R23239 Human parathyroid 8 R23239 Human parathyroid 8 R23245 Human parathyroid 8 R23245 Human parathyroid	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	44	38	38	36	36	ç
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opyl-[LB,K(I noz)-hpTH(1-38 9]-hpTH(1-38 4]-hpTH(1-38 4]-hpTH(1-38 4]-hpTH(1-38 4]-hpTH(1-38 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid 6-parathyroid	R23245	R21239	R34335	R23547	R23522	R21251	R23256	R23368	R21256	R23273	R23434	R23519	R23243	R23453	R23521	R23242	R23241	R23357	R23356	W25687	P30015	810	813	822	908	5
	parathyroid	parathyroi	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid ho	parathyroid	-hPTH(1-38)-	1PTH(1-38	-hPTH(1-	[L8,K(Isop	115 F11 ( F ( C )													

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RESULT
ID R(
AC R(
DT 18
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUNZ) SUNSTAR CHEM IND CO LTD. WPI; 95-157631/21.
R08300 standard; protein; 34 AA.
R08300;
18-FEB-1991 (first entry)
Human parathyroid hormone analogue, Trp12 hPTH(7-34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accelerator is applied by opening the ginging, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the epithelium and accelerates fibre adhesion and regenerates cement. Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure: Page 3: 7pp; Japanese.

The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic amino acids. The accelerate also comprises a cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
periodontal tissue; regeneration; periodontitis; periodontal pocket;
down growth; epithelium; fibre adhesion; cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accelerator for regenerating periodontal tissue - comprises peptide having 3-34 aminoacid residues having connected basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R62432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1993; 045998.
10-FEB-1993; JP-0459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06234653-A.
                                                                                                                                                                                                                                                                                                                                              24 lrkklqd 30
                                                                                                                                                                                                                                                                                           1 LRKKLQD 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 26;
Pred. No. 3.78e+01;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accelerator
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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NW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.
S Homo Saplens.
PN US4958669-A.
PD 06-NOV-1990.
21-APR-1989; 341597.
PR 21-APR-1989; US-191512.
PR 09-MAY-1989; US-191512.
PR 19-754642/47.
PT New para:thyroid hormone analogues - which inhibit hormone activity by binding receptors while not producing second pr messenger molecules.
PT New para:thyroid hormone analogues - which inhibit hormone pr activity by binding receptors while not producing second pr messenger molecules.
PT claim 1; Column 8; 6pp; English.
CC Dut do not stimulate production of secondary messenger molecules.
PS Claim 1; Column 8; 6pp; English.
CC Dut do not stimulate production of prH action, and in diagnosis and treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
CC Analogues may also be used in inhibition of prH action, and inmune diseases eg. allergic inflamation and hyperactive lymphocytes.
Naturally occuring prH levels may also be measured in vitro.
SQ Sequence 34 AA;
Ouery Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.78e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 24 1rkKiqd 30
Qy 1 LRKKLQD 7

Search completed: Thu Jul 30 11:20:26 1998
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MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:19:28 1998; MasPar time 3.06 Seconds 83.440 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-34 (1-7) from US08817547A.pep 52 1 LRKKLQD 7

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.946; Variance 32.007; scale 0.686

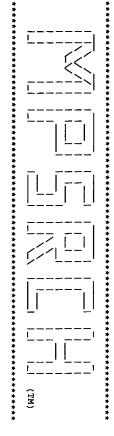
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

11211111111111111111111111111111111111	ult No.
44444555555555555555555555555555555555	Score
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parathyroid hormone 4 parathyroid hormone 4 cyclic parathyroid hormone (parathyroid hormone - parathyroid hormone - parathyroid hormone p parathyroid hormone (parathyroid hormone p parathyroid hor	Description
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45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	24
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polyprotein pp220 pre	myosin heavy chain, n	type I restriction-mo	C3HC4 type zinc finge	uvsH protein - Emeric	glial fibrillary acid	NUVA protein - Emeric	insertion element ISH	4	hypothetical protein	nonstructural polypro	nonstructural polypro	nonstructural polypro	microtubule-associate	probable membrane pro	phenylalaninetRNA l	kinesin-related prote	kinesin-related prote	kinesin-related prote	phosphotransferase sy	steroid 17alpha-monoo	Ca2+/calmodulin-depen
7.11e+01	7.11e+01	7.11e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+01	4.80e+0:							

#submission #cross-refere REFERENCE #authors #book	ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE	RESULT 2 ENTRY TITLE	Db 21 LRKKLQD Qy 1 LRKKLQD	Query Match Best Local Simmatches 7;	2-9 15-25 SUMMARY	COMMENT RESOL COMMENT Deter KEYWORDS	#authors #submission #cross-refere REFERENCE #authors	ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE	RESULT 1 ENTRY TITLE
#SULDIS KOESCH, F.; MAIX, U.C. #SULDISSION SUBMITTED TO THE BROOKHAVEN PROTEIN DATA BANK, June 1996 #CROSS-references PDB:1ZWF #ERENCE TN00318 #BAUTHORS MAIX, U.C. #BAUTHORS MAIX, U.C. #BOOK in Strukturen Verschiedener Parathormonfragmente in Loesung,		12WF #type complete parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -	D 27	Query Match 100.0%; Score 52; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 4.07e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR disease mutation; hormone; signal		nyl-hpth(4 l human pa _name synt	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic



srch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 11:18:09 1998; MasPar time 2.07 Seconds 84.981 Million cell updates/sec

Title:

Sequence: Description: Perfect Score: >US-08-817-547A-34 (1-7) from US08817547A.pep 52 1 LRKKLQD 7

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.054; Variance 26.515; scale 0.869

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length 1	BB	ID	Description	Pred. No.
ب.	52	100.0	115	- 3	PTHY_BOVIN	PARATHYROID HORMONE PR	6.49e-01
" N	л (Л))	100.0	115	ــ بـ	PTHY_CANFA	HORMONE	6.49e-01
~ u	5 U 2 U	100.0	115		PTHY RAT	PARATHYROID HORMONE PR	
u ,	52	100.0	115	٠,	PTHY_HUMAN	HORMONE	: :
6	48	•	621	_	YO4E_MYCTU	L 69.2 KD	:
7	47	•	154	۲	Y17K_SSV1		7.85e+00
8	46	88.5	100	1	YI91_ECOLI	INSERTION ELEMENT IS91	1.26e+01
9	46	88.5	112	٢	YI91_SHIDY	INSERTION ELEMENT IS91	1.26e+01
10	46	88.5	224	1	TCTD_SALTY	TRANSCRIPTIONAL REGULA	1.26e+01
11	46	88.5	447	ר	KCC2_YEAST	CALCIUM/CALMODULIN-DEP	1.26e+01
12	46	88.5	509	H	CPT7_PIG	CYTOCHROME P450 XVIIA1	1.26e+01
13	46	88.5	637	۳	PTMA_ECOLI	PTS SYSTEM, MANNITOL-S	1.26e+01
14	46	88.5	745	۲	KATB_ARATH	KINESIN-LIKE PROTEIN B	1.26e+01
15	46	88.5	754	μ	KATC_ARATH	KINESIN-LIKE PROTEIN C	1.26e+01
16	46	88.5	793	Н	KATA_ARATH	KINESIN-LIKE PROTEIN A	1.26e+01
17	46	88.5	806	ب	SYFB_MYCGE	PHENYLALANYL-TRNA SYNT	1.26e+01
18	46	88.5	1231	μ.	KIF4 MOUSE	KINESIN-LIKE PROTEIN K	1.26e+01
19	46	88.5	2492	Ь	POLN_EEVVT	NONSTRUCTURAL POLYPROT	1.26e+01
20	46	88.5	2492	\vdash	POLN_EEVVP	NONSTRUCTURAL POLYPROT	1.26e+01
21	46	88.5	2492	Н	POLN_EEVV3	NONSTRUCTURAL POLYPROT	1.26e+01
22	45	86.5	229	H	YXDJ_BACSU	HYPOTHETICAL 26.6 KD S	2.02e+01
23	45	86.5	428	_	GFAP_BOVIN	GLIAL FIBRILLARY ACIDI	2.02e+01

45	44	43	42	41	40	39	ა 8	37	3 6	ა წ	34	33	32	31	30	29	28	27	26	25	24
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84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	86.5	86.5	86.5
2843	752	669	630	617	565	470	463	461	458	453	450	444	335	314	310	182	110	100	4725	430	430
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APC_HUMAN	HPR1_YEAST	YMS2_YEAST	Y019_METJA	ASMA_ECOLI	NO56_SOYBN	BFR1_YEAST	VIM4_XENLA	VIME_ONCMY	IF3T_TORCA	OP2_MAIZE	VIMB_CARAU	CIT1_KLEPN	HIS9_YEAST	GCR_SHEEP	SYNK_ARATH	Y922_HAEIN	PTCA_BACSU	RR14_PORPU	DYHC_DICDI	GFAP_MOUSE	GFAP_RAT
ADENOMATOUS POLYPOSIS	HPR1 PROTEIN.	HYPOTHETICAL 76.2 KD P	HYPOTHETICAL PROTEIN M	ASMA PROTEIN PRECURSOR	LATE NODULIN 56 (N-56)	NUCLEAR SEGREGATION PR	VIMENTIN 4.	VIMENTIN.	TYPE III INTERMEDIATE	OPAQUE-2 REGULATORY PR	VIMENTIN BETA.	CITRATE-PROTON SYMPORT	HISTIDINOL-PHOSPHATASE	GLUCOCORTICOID RECEPTO	SYNTAXIN-RELATED PROTE	HYPOTHETICAL LIPOPROTE	PTS SYSTEM, CELLOBIOSE	CHLOROPLAST 30S RIBOSO	DYNEIN HEAVY CHAIN, CY	GLIAL FIBRILLARY ACIDI	GLIAL FIBRILLARY ACIDI
3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20c+01	3.20e+01	3.20e+01	2.02e+01	2.02e+01	2.02e+01

RRARRARRARRARRARRARRARRARRARRARRARRARRA	RN RA	R R R R R R R R R R R R R R R R R R R	RRA RRA RRA	RESULT ID P AC P DT 2 DT 2 DT 0 DE P GN P
SEQUENCE OF 32-115. SEQUENCE OF 32-115. MEDLINE; 71076162. MIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F., AURBACH G.D., POTTS J.T. JR.; HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970). [7] SEQUENCE OF 32-115. MEDLINE; 71063634.	SEQUENCE FROM N.A. MEDLINE; 84.262483. WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.; GENE 28:319-329(1984). [5] SEQUENCE OF 26-115. MEDLINE; 74.142666. HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTWANN H.T., POTTS J.T. JR., PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).	SEQUENCE FROM N.A. MEDLINE; 82037785. WEAVER C.A., GORDON D.F., KEMPER B.; PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981). 31 SEQUENCE FROM N.A. MEDLINE; 83105964. MEAVER C.A., GORDON D.F., KEMPER B.; MOL. CELL. ENDOCRINOL. 28:411-424(1982).	BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; ARTIODACTYLA. [1] SEQUENCE FROM N.A. MEDLINE; 80056617. KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A., POTTS J.T., JR., RICH A.; PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979). [2]	TTY_BOVIN STANDARD; PRT; 115 AA. PTYY_BOVIN STANDARD; PRT; 115 AA. P01268; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH). PTH.

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Best Local S
Matches
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δÃ
                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNTHESIS OF 32-65. MEDLINE; 71091588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTHY_CANFA STANDARD; PRT; 115 AA.

P52212;

P52212;

01-OCT-1996 (REL. 34, CREATED)

01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                 SIGNAL
PROPEP
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE PARATHYROID;

MEDLINE; 9536966.

ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

DEWILLE J.W., CAPEN C.C.;

GENE 160:241-243(1995).

GE
                                                                                                                                                                                                                                                  PROSITE; PS00335; PARATHYROID; 1. HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 LRKKLQD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LRKKLOD 7
                              55 LRKKLQD 61
    LRKKLQD 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%;
Similarity 100.0%;
7; Conservative
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115 AA;
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26
32
115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
31
115 PARATHYROID HORMONE.
106 V -> G (IN REF. 4).
12980 MW; 673EA5F2 CRC32;
                                                                                                                                                                     25
31
B1
115
P4
; 12957 MW;
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U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 1; Length 115;
Pred. No. 6.49e-01;
0; Mismatches 0; Indels
                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
W; 16ED0EBC CRC32;
                                                                                         Score 52; DB 1; Length 115;
Pred. No. 6.49e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AA.
                                                                                                                                     Length 115;
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Search completed: Thu Jul 30 11:18:16 1998 Job time: 7 secs.

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(MT)
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MPsrch_pp 9 protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 11:18:33 1998; MasPar time 3.62 Seconds 81.362 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-817-547A-34 (1-7) from US08817547A.pep 52

Title:

1 LRKKLQD 7

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl5 1:sp fur

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_bhage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

Statistics: Mean 22.212; Variance 26.174; scale 0.849

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12			Q	œ	7		υ	4	w	N	ч	Result No. Score
46 8	46 8	46 8	46 8	46 88	46 8		46 88	47 90		47 9		48 92	48 9	51 9	51 9	51 9	52 10	52 100	:
- co	8.5	8.5				8.5	8.5	0.4	0.4	0.4	0.4	2.3	2.3	8.1	8.1	8.1	0.0	0.0	Query Match Le
899 1034	434	316	263	231	134	122	122											105]	Length I
., <u> </u>	μ.	9	ø	_	9	9	9	5	ဖ	œ	φ	w	œ	ω	œ	ω	9	0	DB.
Q06132	P78918	Q56689	P96187	Q05436	P75679	032286	P71288	Q63618	029516	Q40969	P73917	Q18255	004471	Q40700	P93468	Q40970	032491	Q63473	IJ
CHROMOSOME XII COSMID	FISSION YEAST (FRAGMEN	TRANSMEMBRANE TRANSCRI	HRPG.	CAM KINASE II (FRAGMEN	FROM BASES 263572 TO 2	YXZC PROTEIN.	HYPOTHETICAL IS911 PRO	ESPIN.	DNA PRIMASE, PUTATIVE.	PUTATIVE MADS-BOX FAMI	HYPOTHETICAL 15.4 KD P	COSMID C27D9.	SIMILAR TO SACCHAROMYC	BOX PROTEIN.	MADS-BOX FAMILY TRANSC	PUTATIVE MADS-BOX FAMI	PUTATIVE N6-ADEININE S	PARATHYROID HORMONE (F	Description
1.72e+01	1.72e+01	1.72e+01	1.72e+01	1.72e+01	1.72e+01	1.72e+01	1.72e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	6.55e+00	6.55e+00	1.46e+00	1.46e+00	1.46e+00	8.70e-01	8.70e-01	Pred. No.

5 2493 11 Q66594 NONSTRUCTURAL 5 2497 11 Q88978 NONSTRUCTURAL 5 153 9 Q52560 ORF WITHIN ISI 5 192 9 Q47977 INSERTION SEQU 5 226 9 P96373 KDPE. 5 226 9 P96373 KDPE. 5 275 9 Q48291 PUTATIVE TRANS 5 356 1 Q00178 DNA REPAIR AND 6 1 Q00218 DNA REPAIR AND 7 1 Q00138 DNA REPAIR AND 7 1 Q00138 DNA REPAIR AND 7 1 Q00138 DNA REPAIR AND 7 1 Q00318 DNA PROTEIN PROBEIL 7 1	45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	
8.5 2493 11 Q66594 NONSTRUCTURAL POLYER 8.5 2497 11 Q88978 NONSTRUCTURAL POLYER 8.5 2497 11 Q88978 NONSTRUCTURAL POLYER 8.5 2497 11 Q88978 NONSTRUCTURAL POLYER 8.5 2497 11 Q88970 OF WITHIN IS1240. 6.5 192 9 Q47977 INSERTION SEQUENCE I Q47977 INSERTION SEQUENCE I Q48991 PUTATIVE TRANSPOSASE 6.5 275 9 Q48991 PUTATIVE TRANSPOSASE PUTATIVE TRANSPOSASE A43 1 Q02399 DNA REPAIR AND RECON G.5 477 1 Q00183 DNA REPAIR AND RECON G.5 477 1 Q00183 DNA REPAIR AND RECON G.5 1939 9 Q28565 TYPE I RESTRICTION-PG.5 1939 10 Q63731 NEURONAL MYOSIN HEAVER G.5 1939 10 Q63731 NEURONAL MYOSIN HEAVER G.5 2475 11 Q08338 POLYPROTEIN PP220. 6.5 1939 10 Q63731 NEURONAL MYOSIN HEAVER G.5 237 3 Q21772 NADS BOX PROTEIN (FF 4.6 237 3 Q21772 MADS BOX PROTEIN (FF 4.6 249 8 Q41835 BOX	44	44	44	44	44	44	44	44	45	45	<u>4</u> 5	45	45	45	45	45	45	45	45	45	45	45	46	46	ć
93 11 066594 NONSTRUCTURAL POLYPH 97 11 088978 NONSTRUCTURAL POLYPH 97 11 088978 NONSTRUCTURAL POLYPH 97 11 088978 NONSTRUCTURAL POLYPH 97 10 02596 ORF WITHIN IS1240. 19 02456 ORF WITHIN IS1240. 19 024573 KDPE. 19 024572 MADS-BOX PROTEIN AGI 19 0248291 PUTATIVE TRANSPOSASE 19 0248291 PUTATIVE TRANSPOSASE 19 0248291 DNA REPAIR AND RECON 19 0240183 DNA REPAIR AND RECON 19 028565 TYPE I RESTRICTION-19 10 028565 TYPE I RESTRICTION-19 10 026731 NEURONAL MYOSIN HEAV 10 063731 NEURONAL MYOSIN HEAV 11 008358 POLYPROTEIN (FF 10 026731 POLYPROTEIN (FF 10 026928 MADS BOX PROTEIN (FF 10 026151 SMAPHORIN I (M-SENAL 10 026151 SMAPHORIN I (M-SENAL 11 0261151 SMAPHORIN I (M-SENAL 12 026151 SMAPHORIN	4	4	4	4	4	٠.		4	σ.	<u>ه</u>	σ,	σ.	<u>ب</u>	5	<u>ه</u>	<u>ი</u>	<u>ი</u>	σ.	σ.	σ,	σ.	5	ω.	8	
Q66594 NONSTRUCTURAL POLYER Q88978 NONSTRUCTURAL POLYER Q89978 NONSTRUCTURAL POLYER Q89978 NADS-BOX PROTEIN AGI Q89978 NEPAIR AND RECON Q17750 C06G3.9 PROTEIN C06G3.9 PROTEIN C06G3.9 PROTEIN Q89565 TYPE I RESTRICTION-N Q89565 NTYPE I RESTRICTION-N Q89731 NEURONAL MYOSIN HEAV Q89731 NEURONAL MYOSIN HEAV Q89738 POLYPROTEIN (FF Q84P04 Q81151 Q84P04 Q84151 SEMAPHORIN I NTERACTI Q84015 DNA BINDING PROTEIN Q84151 SEMAPHORIN I NTERACTI Q84015 DNA BINDING PROTEIN Q84151 SEMAPHORIN I NTERACTI Q84015 DNA BOX POTEIN Q84151 SEMAPHORIN I NTERACTI Q84015 DNA BENOMATOUS POLYPOSI	2829	914	834	437	249	237	237	223	3212							443	356	275	258	226	192	153	7	93	•
A NONSTRUCTURAL POLYPE B NONSTRUCTURAL POLYPE B NONSTRUCTURAL POLYPE B NONSTRUCTURAL POLYPE B NONSTRUCTURAL POLYPE INSERTION SEQUENCE I INSERTION SEQUENCE I INSERTION PROTEIN AGI PUTATIVE TRANSPOSASE DNA REPAIR AND RECON DNA REPAIR AND RECON DNA REPAIR AND RECON CO6G3.9 PROTEIN. TYPE I RESTRICTION-PORE/IN HEAV POLYPEII PEZZO. ORF1130. TYPE I RESTRICTION-POLYPEOTEIN (FF MADS HOX PROTEIN (FF MADS HO	12	N	10	œ	œ	œ	w	Н	ω	11	10	ဖ	9	ω	Ь	ᆫ	Н	9	œ	9	9	9	11	11	ŀ
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	ADENOMATOUS POLYPOSIS		I (M-SEMA	BINDING PROTEIN	BOX	BOX PROTEIN	R06C7.2.	G4P04.	T08G11.1.	POLYPROTEIN PP220.	NEURONAL MYOSIN HEAVY	ORF1130.	н	C06G3.9 PROTEIN.			REPAIR AND		PROTEIN	KDPE.		ORF WITHIN IS1240.			WOND THE POST OFFICE

₽ X	R	RP	RN	გ	გ	SO	B	TC	ΤŢ	Ţ	AC.	Ü	RESULT	Qy	į	D.	Ma Be	SO	T)	DR :	R.	RA	200	ŖΡ	RN	റ്റ	റ്റ	တ္ထ	GN	DE	ij	ဌ	D ;	Å	ij	RESULT
MEDILINE; 96118688. HARING V., BILLINGTON S.J., WRIGHT C.L., HUGGINS A.S., KATZ M.E.,	STRAIN-AI98;	SEQUENCE FROM N.A.	[1]	BACTEROIDACEAE.	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;	BACTEROIDES NODOSUS (DICHELOBACTER NODOSUS).	PUTATIVE N6-ADEININE SPECIFIC METHYLTRANSFERASE.	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	(TREMBLREL.	(TREMBLREL.		032491 PRELIMINARY; PRT; 929 AA.		1 LRKKLQD 7		45 LRKKLOD 51	Query Match 100.0%; Score 52; DB 10; Length 105; Best Local Similarity 100.0%; Pred. No. 8.70e-01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;		, M548	TECHNOL. 21:228-229(1)	SCHMELZER H.J., GROSS G., MAYER H.;	TISSUE-THYROID, AND PARATHYROID;	SEQUENCE FROM N.A.	[1]		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	RATTUS NORVEGICUS (RAT).		HORMONE (FRAGMENT).	(TREMBLREL. 05, LAST ANNOTATIO	(TREMBLREL: 01,	01-NOV-1996 (TREMBLREL, 01, CREATED)		O63473 PRELIMINARY; PRT; 105 AA.	

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RA ROOD J.I.;

MICROBIOLOGY 141:0-0(0).

DR EMBL, UT00447, 62317805; -

SQ SEQUENCE 929 AA: 106474 MW; 4085E117 CRC32;

SEQUENCE 929 AA: 106474 MW; 4085E117 CRC32;

Best Local Similarity 100.0%; Fred. No. 8.70e-01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

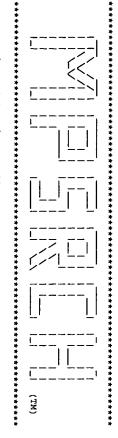
MACLE LERKLOD 48

JIHILI

QY 1 LERKLOD 7

Search completed: Thu Jul 30 11:19:10 1998

JOb time: 37 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. 9 1 Thu Jul 30 11:22:40 1998; MasPar time 2.49 Seconds 30.840 Million cell updates/sec

Perfect Score: Description: >US-08-817-547A-36 (1-5) from US08817547A.pep 39 1 LRKKL 5

Title:

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.364; Variance 43.704; scale 0.329

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

escription cccelerator peptide b L8,018,A29,E30,I31] Thr16]hPTH (1-34). Thr26]hPTH (1-34). Sopropyl-[L8,K(Isopr D-Asa3)hPTH(1-34)- yclised [Nle 8,18, T yclised [Nle 8,18, T yclised [Nle 8,18, T yclised [Nle 16, T yclised [Nle 7, T uman PTH analogue [C D-Glu19]-hPTH(1-36)- L8,010,A16,018]-hPTH Asa1]-hPTH(1-36) Met(02)18]-hPTH(1-36)- Met(102)18]-hPTH(1-36)-

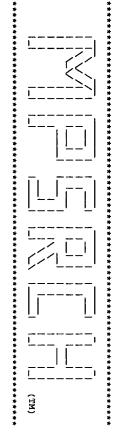
4 5	44	43	42	41	40	39	38	37	36	ဌ	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	2
39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	ú
00.	8	00.	00.	80.	80.	8	8	8	100.0	8	8	80.	8	8	8	8	8	8	8	8	8	8	8	8	č
496	479	289	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	44	38	38	38	38	38	ú
27	27	ر.	4	4	4	4	S	4	4	4	4	տ	4	4	4	4	4	27	26	9	9	φ	φ	φ	ď
39	39	83	19	46	R23357	35	\mathbf{r}	σ	R21160	œ	œ	O	v.	~	~	~	339	2568	8	803	812	802	810	82	9
Mch5 protein.	4	VP1 Asp101Glu of HRV	Human parathyroid hor	Porcine parathyroid h	Bovine parathyroid ho	Bovine parathyroid ho	Parathyroid	Ġ,	Human parathyroid hor	à	Ω	Oxidation resistant [Bovine parathyroid ho	parathyroid	Porcine parathyroid h	ne parathyroid	Human parathyroid hor	parathyroid h	6]-hPTH(1-38)	[Met17]-hPTH(1-38)-OH]-hPTH(1-38)-	4]-hPTH(1	(1-38)-	[Argss] "nrTH(I sa) "OH
.76e+0	.76e+0	.76e+0	.76e+0	.76e+0	.76e+0	.76e+0	.76e+0	.76e+0	3.76e+02	. 76	.76e+0	.76e+0	.76e+0	. 76	.76e+0	.76e+0	.76e+0	.76e+0	.76e+0	.76e+0	•	.76e+0	. 76e	.76e	3./betua

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RESULT
ID RE
AC RE
DT 20
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                                                                                                                                                  ₽
                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                              Disclosure; Page 3; 7pp; Japanese.

The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic amino acids. The accelerato also comprises a cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The accelerator is applied by opening the gingiva, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the epithelium and accelerates fibre adhesion and regenerates cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-1994.
10-FEB-1993;
10-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva; periodontal tissue; regeneration; periodontitis; periodontal pocket; down growth; epithelium; fibre adhesion; cement.
R58040;
20-SEP-1994 (first entry)
[L8,Q18,A29,E30,I31]-hPTH(1-34)-OH
                                                R58040 standard;
                                                                                                                                                                                                                                                  epithelium and ac
Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Accelerator for regenerating periodontal tissue - comprises peptide having 3-34 aminoacid residues having connected basic aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-1993; 04-5998.
10-FEB-1993; JP-04-5998.
(SUMZ) SUNSTAR CHEM IND CO LTD.
WPI; 95-157631/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
J06234653-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R62432 standard;
R62432;
                                                                                                                                                24 lrkkl 28
                                                                                                                   1 LRKKL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                     34
                                                                                                                                                                                Score 39; DB 26;
Pred. No. 3.76e+02;
0; M1smatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
A
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                                                                                                                                                                                    0;
                                                                                                                                                                                                               Length 34;
                                                                                                                                                                                    Indels
                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                 accelerator
                                                                                                                                                                                    Gaps
                                                                                                                                                                                    0
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pn 02-FEB-1994.
pp 02-FEB-1994.
pp 02-FEB-1994.
pp 02-FEB-1994.
pp 12-UTL-1993; 0B-015009.
pr 15-UTL-1992; GB-026415.
pr 15-UTL-1992; GB-026615.
pr 15-UTL-1992; GB-026651.
pr 23-DEC-1992; GB-026651.
pr 23-DEC-1992; GB-001691.
pr 28-UNN-1993; GB-001691.
pr 14-APR-1993; GB-001692.
pr 14-APR-1993; GB-001693.
pr 14-APR-1993; GB-008033.
pr 13-APR-1993; GB-001691.
pr 13-APR-1
                                                                                                                                                                                                                                         SCCCCC P P P P P
δã
                                                            В
                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
Synthetic.
24 lrkkl 28
|||||
1 LRKKL 5
                                                                                                                            Score 39; DB 9; Length 34; pred. No. 3.76e+02; 0; Mismatches 0; Indels
                                                                                                                                            Indels
                                                                                                                                            0;
                                                                                                                                               Gaps
                                                                                                                                                      0
```

search completed: Thu Jul 30 11:22:55 1998
Job time : 15 secs.



erch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:22:05 1998; MasPar time 2.97 Seconds 61.502 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-36 (1-5) from US08817547A.pep 39 1 LRKKL 5

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 20.005; Variance 26.164; scale 0.765

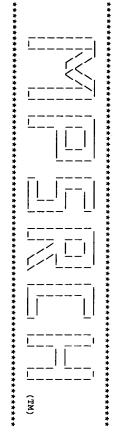
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Query Match Length	DB.	₽	Description	Pred. No.
_	39	100.0	34	5	12WE	parathyroid hormone (1.53e+02
N	39	100.0	34	S	1ZWG		1.53e+02
ω	39	•	34	IJ	1HTH	+	1.53e+02
4	39	100.0	34	σ	1ZWA	parathyroid hormone (1.53e+02
σ	39	100.0	34	Ç	1ZWF	parathyroid hormone 4	1.53e+02
6	39	100.0	35	Ų	1ZWD	parathyroid hormone (1.53e+02
7	39	100.0	36	Ŋ	12WB	parathyroid hormone (1.53e+02
&	39	100.0	37	υ	1HPH	parathyroid hormone f	1.53e+02
9	39	100.0	37	Ç	1ZWC	parathyroid hormone (1.53e+02
10	39	100.0	73	u	1FIPA	Fis protein (factor f	1.53e+02
11	39	100.0	73	u	3FISA	_	1.53e+02
12	39	100.0	73	Ģ	3FISB	DNA-binding protein f	1.53e+02
13	39	100.0	73	u	1FIPB	_	1.53e+02
14	39	100.0	74	Ç	1FIAB2	Fis protein (factor f	1.53e+02
15	39	100.0	75	S	1FIAA2	Fis protein (factor f	1.53e+02
16	39	100.0	89	Ç	1F36B	fis mutant K36E, chai	1.53e+02
17	39	100.0	271	Çī	1RUFA2	rhinovirus 14 mutant	1.53e+02
18	39	100.0	273	G	1RUCA	rhinovirus 14 mutant	1.53e+02
19	39	100.0	273	ر.	1HRVA	rhinovirus 14 (hrv14)	1.53e+02
20	39	100.0	273	տ	1RUHA	rhinovirus 14 mutant	1.53e+02
21	39	100.0	273	σ	1RUGA	rhinovirus 14 mutant	1.53e+02
22	39	100.0	273	σ	1RHIA	rhinovirus 3 coat pro	1.53e+02
23	39	100.0	273	G	1VRHA	rhinovirus 14 mutant	1.53e+02

45	44	43	42	41	40	39	38	37	36	35 5	34	ယ	3 2	31	30	29	28	27	26	25	24
39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	3
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	T00.0
500	500	492	492	273	273	273	273	273	273	273	273	273	273	273	273	273	273	273	273	273	2/3
S	ហ	Ç	σ	v	Ç	υ	Ģ	u	ហ	v	v	ű	σı	IJ	ഗ	ហ	v	u	v	G	U
1ECGB	1ECFB	1ECFA	1ECGA	1R08A	1HRIA	1RU1A	2RR1A	2HWCA	2R04A	1R09A	2HWBA	2R06A	2RS3A	2RS5A	4RHVA	2RM2A	2RS1A	2R07A	1RUJA	1RUDA	LACEA
glutamine phosphoribo	glutamine phosphoribo	glutamine phosphoribo	glutamine phosphoribo	coat protein VP1 (wit	coat protein VP1 (wit	rhinovirus 14 mutant	coat protein VP1 (wit	1 VP1 r	coat protein VP1 (wit	coat protein VP1 (wit	coat protein VP1 muta	coat protein VP1 (wit	VP1	coat protein VP1 (wit	coat protein VP1, cha	coat protein VP1 (wit	coat protein VP1 (wit	coat protein VP1 (wit	rhinovirus 14 mutant	rhinovirus 14 mutant	TUINOVII BY MULCANC
1.53e+0;	1.53e+02	1.53e+02	1.53e+0	1.53e+0	1.53e+0:	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+0	1.53e+02	1.53e+02	1.53e+02	L. DUETO.

Search completed: Thu Jul 30 11:22:22 1998 Job time : 17 secs. В COMMENT KEYWORDS FEATURE 2-9 15-25 SUMMARY δÔ Query Match 100.0%; Score 39; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 1.53e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 21 LRKKL 25 |||| 1 LRKKL 5 Determination: NMR
disease mutation; hormone; signal #region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34 #molecular weight 4128 #checksum 5508 0;



Psrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 11:20:45 1998; MasPar time 2.01 Seconds 62.459 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-36 (1-5) from US08817547A.pep 39 1 LRKKL 5

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.052; Variance 21.024; scale 1.001

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	% Query Match L	Length D	BB	Ħ	Description	Pred. No.
ъ	39	100.0	9.6	۲;	FIS_ECOLI	FACTOR-FOR-INVERSION S	4.38e+01
2	39	100.0	100	-	91	9	4.38e+01
ω	39	100.0	112	_	YI91_SHIDY	ELEMENT IS9	4.38e+01
4	39	100.0	115	۲	PTHY_CANFA	PARATHYROID HORMONE PR	
· G	39	100.0	115	۲	PTHY_HUMAN	PARATHYROID HORMONE PR	4.38e+01
0	39	100.0	115	-	PTHY_BOVIN	PARATHYROID HORMONE PR	4.38e+01
7	39	100.0	209	_	VS10_ROTBS	MINOR OUTER CAPSID PRO	4.38e+01
. &	39	100.0	209	_	RR3_GRATE	CHLOROPLAST 30S RIBOSO	4.38e+01
	39		213	_	URK_MYCPN	URIDINE KINASE (EC 2.7	4.38e+01
10	39	100.0	224	. ш	TCTD_SALTY	TRANSCRIPTIONAL REGULA	
<u>_</u>	3 9	T00.0	229	-	YXDJ_BACSU	HYPOTHETICAL 26.6 KD S	4.38e+01
12	39		242	_	RSTA_ECOLI	TRANSCRIPTIONAL REGULA	4.38e+01
13	39		310	_	SYNK_ARATH	SYNTAXIN-RELATED PROTE	4.38e+01
14	39	100.0	330	1	YXAQ_BACSU	HYPOTHETICAL 37.5 KD P	4.38e+01
15	39	•	334	-	YHO5_YEAST	HYPOTHETICAL 37.9 KD P	4.38e+01
16	39		353	_	Y613_METJA	PUTATIVE ENDONUCLEASE	4.38e+01
17	39	100.0	360	Н	HIS8_LACLA	HISTIDINOL-PHOSPHATE A	4.38e+01
18	39	100.0	366	_	SYY_SULSO	TYROSYL-TRNA SYNTHETAS	4.38e+01
19	39	•	435	Н	MRP_MYCLE	MRP PROTEIN HOMOLOG.	4.38e+01
20	39	100.0	437	۲	SECY_STRGB	PREPROTEIN TRANSLOCASE	4.38e+01
21	39	100.0	437	μ	SECY_STRGR	PREPROTEIN TRANSLOCASE	4.38e+01
22	39	100.0	437	μ.	SECY_STRSC	PREPROTEIN TRANSLOCASE	4.38e+01
23	39	100.0	437	1	SECY_STRLI	PREPROTEIN TRANSLOCASE	4.38e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
39	39	39	39	ω 9	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
100.0	100.0	8	100.0	100.0	100.0	100.0	100.0	100.0	•	100.0	٠	•	100.0	٠	100.0	•	100.0	00.	100.0	80.	100.0
2492	2492	2492	1032	1031	926	806	800	754	745	744	517	517	504	501	496	496	479	459	455	451	444
μ	<u>, , , , , , , , , , , , , , , , , , , </u>	ب	μ	_	بر	ш	н	۲	Н	بر	Н	Н	_	_	ب	_	Н	ш	Н	,	Ь
POLN_EEVVT	POLN_EEVV3	POLN_EEVVP	YQ53_CAEEL	RAD2_YEAST	PQQL_HAEIN	SYFB_MYCGE	RR3_CHLEU	KATC_ARATH	KATB_ARATH	NU85_YEAST	PUR1_RAT	PUR1_HUMAN	PUR1_ECOLI	UVS2_NEUCR	RECQ_BACSU	SRM_MOUSE	ICE8_HUMAN	NU4M_HYLLA	YNU6_YEAST	TRPC_BUCAP	PURA_SYNY3
_	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	HYPOTHETICAL 117.1 KD	DNA REPAIR PROTEIN RAD	PROBABLE ZINC PROTEASE	PHENYLALANYL-TRNA SYNT	CHLOROPLAST PUTATIVE 3		KINESIN-LIKE PROTEIN B	NUCLEOPORIN NUP85 (NUC	AMIDOPHOSPHORIBOSYLTRA	AMIDOPHOSPHORIBOSYLTRA	AMIDOPHOSPHORIBOSYLTRA	UVS-2 PROTEIN.	ATP-DEPENDENT DNA HELI	TYROSINE-PROTEIN KINAS	CASPASE-8 PRECURSOR (E	NADH-UBIQUINONE OXIDOR	HYPOTHETICAL 51.6 KD P	INDOLE-3-GLYCEROL PHOS	ADENYLOSUCCINATE SYNTH
	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01				4.38e+01	4.38e+01	4.38e+01		4.38e+01	4.38e+01

R R R R R R	R R R R R R R R R R R R R R R R R R R	RA RA	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	R R R R R R	R R R R R R R R R	S S S S S S S S S S S S S S S S S S S	RESULT FAC PODT 0
FUNCTION. SPECIES-E.COLI; MEDLINE; 91006075. MEDS W., THOMPSON J.F., NEWLANDS J.T., GOURSE R.L.; ROSS W., THOMPSON J.F., NEWLANDS J.T., GOURSE R.L.;	SEQUENCE FROM N.A. SPECIES-S.TYPHIMURUM; STRAIN-LT2; MEDLINE; 95238273. MEDLINE; 95238273. OSUNA R., LIENAU D., HUGHES K.T., JOHNSON R.C.; J. BACTERIOL. 177:2021-2032(1995).	- m > m o -	J. BACTERIOL. 174:8043-8056(1992).	SEQUENCE FROM N.A. SPECIES-E.COLI; SPECIES-E.COLI; MEDLINE; 88247997. KOCH C., VANDERKERCKHOVE J., KAHMANN R.; FROC. NATL. ACAD. SCI. U.S.A. 85:4237-4241(1988).	[1] SEQUENCE FROM N.A., AND SEQUENCE. SPECIES-E.COLI; MEDLINE; 88217925. JOHNSON R.C., BALL C.A., PFEFFER D., SIMON M.I.; PROC. NATL. ACAD. SCI. U.S.A. 85:3484-3488(1988).	BINDING PROTEIN) (FIS PROTEIN). FIS. ESCHERICHIA COLI, AND SALMONELLA TYPHIMURIUM. PROKARYOTH, GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.	1 SECOLI STANDARD; PRT; 98 AA. 11078; P37404; 1-JUL-1989 (REL. 11, CREATED) 1-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE) 1-JUL-1989 (REL. 35, LAST ANNOTATION UPDATE) 1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

FUNCTION

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RESULT 2
ID Y191_ECOLI
AC P39212;
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Best Local S
Matches
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EMBL; J03245; G145971; - .
EMBL; J03816; G145973; - .
EMBL; W95784; G145977; - .
EMBL; U18997; G606202; - .
EMBL; U18997; G606202; - .
EMBL; U03101; G424092; - .
PIR; A32142; DNECES.
PIR; A32142; DNECES.
PIR; A15344; S15344; S1544; S1
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WOLD S., CROOKE E., SKARST!
NUCLEIC ACIDS RES. 24:3527
[8]
NUTAGENESIS, AND DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-E.COLI;

SEDITINE; 92318362.

NOSITREWA D., GRANZIN J., STOCK D., CHOE H.-W., LABAHN J., SAENGER W.;

NOSITREWA D., GRANZIN J., STOCK D., CHOE H.-W., LABAHN J., SAENGER W.;

J. MOL. BIOL. 226:209-226(1992).

1. FUNCTION: ACTIVATES RIBOSOWAL RNA TRANSCRIPTION. PLAYS A DIRECT ROLE IN UPSTREAM ACTIVATION OF RRNA PROMOTERS. BINDS TO A RECOMBINATIONAL ENHANCER SEQUENCE THAT IS REQUIRED TO STIMULATE HIN-MEDIATED DNA INVERSION. PREVENTS INITIATION OF DNA REPLICATION
                                                                                                                                                                                                                                                                                                        TURN
HELIX
TURN
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MEDLINE; 91.09505.
KOSTREWA D., GRANZIN J., KOCH C., CHOE H.-W., RAGHUNATHAN S., WOLF
LABAHN J., KAHMANN R., SAENGER W.;
NATURE 349:178-180(1991).
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OSUNA R., FINKEL S.E., JOHNSON R.C.;
EMBO J. 10:1593-1603(1991).
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYGENE; SG1
DNA-BINDING;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECOGENE;
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                                                                                                        88 LRKKL 92
|||||
1 LRKKL 5
                                                                                                                                                                                                                 Match 100.0%; Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1FIP; 14-FEB-95.
3FIS; 31-OCT-93.
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                        STANDARD;
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24:3527-3532(1996).
                                                                                                                                                                                                                                                                                  11240 MW;
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441
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72
72
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                                                                                                                                                                                           Score 39; DB 1; L. Pred. No. 4.38e+01; 0; Mismatches 0
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H-T-H MOTIF.
                        PRT;
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Best Local S
Matches
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NUCLEIC ACIDS RES. 23:2105-2119(1995).

EMBL; U14003; G537124; -.

EMBL; AE000499; G1790735; -.

HYPOTHETICAL PROTEIN; TRANSPOSABLE ELEMENT.

SEQUENCE 100 AA; 11558 MW; 3827E6B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INSERTION ELEMENT IS911 HYPOTHETICAL 11.6 KD PROTEIN (0100).
ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 95334365;
BURLAND V.D., PLUNKETT G. III,
                                                                                          82 LRKKL 86
                                                                                                                                                                                         / Match 100.0%;
Local Similarity 100.0%;
nes 5; Conservative
\vdash
     LRKKL 5
                                                                                                                                                                                         Score 39; DB 1; 1
Pred. No. 4.38e+01,
0; Mismatches (
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                                                                                                                                                                                                                                                                                    Length 100;
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                                                                                                                                                                                              Indels
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Search completed: Thu Jul 30 11:20:51 1998 Job time: 6 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 11:21:10 1998; MasPar time 3.54 Seconds 59.507 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-817-547A-36 (1-5) from US08817547A.pep 39 1 LRKKL 5

Title:

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics; 20.197; Variance 20.875; scale 0.968

re y.-a.er than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20	19	18	17	16	15	14	13	12	11	10	9	80	7	o	ហ	4	ω	2	-	Result
39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match 1
480	470 1	459	459	459	459	437 1	434		360	346	299 1		259	231	231	218	199	105 1	65	Length DB
N	0	σ	σ	σ	σ	-	۳	10	9	9	μ	11	9	ш	9	9	9	10	ω	. iii
015519	008854	021714	021698	021706	021845	036416	P78918	Q63701	034130	029648	Q84775	Q84737	028703	Q05436	034951	029263	027967	Q63473	Q24890	Ħ
CASPER.	TRAF-INTERACTING PROTE	NADH DEHYDROGENASE SUB	NADH DEHYDROGENASE SUB	NADH DEHYDROGENASE SUB	NADH DEHYDROGENASE SUB	ORF66.	FISSION YEAST (FRAGMEN	CATHEPSIN E PRECURSOR.	HISC.	LPS GLYCOSYLTRANSFERAS	14 (HRV-14) RNA SEQUEN	TYPE 14 (HRV14), COMPL	CONSERVED HYPOTHETICAL	CAM KINASE II (FRAGMEN	SIGNAL TRANSDUCTION RE	HYPOTHETICAL 24.6 KD P	CONSERVED HYPOTHETICAL	PARATHYROID HORMONE (F	ANTIGEN B (FRAGMENT).	Description
5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
2497	2493	2493	1616	1338	1335	1282	1115	1005	954	939	938	929	899	885	880	855	836	808	775	764	627	529	495	481
1	11	H	11	N	ω	N	11	N	N	10	2	ø	μ	N	10	11	10	9	۳	ω	ဖ	N	ဖ	10
Q88978	Q66592	Q66594	P90211	014765	Q17250	Q14692	Q83484	Q13625	015326	Q62784	Q13187	032491	Q06132	Q13122	P97693	Q82081	Q63618	Q58937	013971	Q22598	030244	Q12892	027663	035707
NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	180K PROTEIN.	ALDEHYDE OXIDASE.	XANTHINE DEHYDROGENASE	KIAA0187 PROTEIN.	130K PROTEIN.	BBP/53BP2.	INOSITOL POLYPHOSPHATE	INOSITOL POLYPHOSPHATE	INOSITOL POLYPHOSPHATE	PUTATIVE N6-ADEININE S	CHROMOSOME XII COSMID	100 KDA COACTIVATOR.	P105 COACTIVATOR.	COAT PROTEIN (FRAGMENT	ESPIN.	95.6 KD	ICAL	т19н5.1.	HYPOTHETICAL 72.0 KD P	P53-BINDING PROTEIN (F	PHOSPHOSERINE PHOSPHAT	FLICE-LIKE INHIBITORY
	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	٠	•		•	5.95e+01	5.95e+01	٠	٠	5.95e+01	٠	5.95e+01	٠	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01

ALIGNMENTS

RF RC RF	20002	RESULT ID O DT	δλ P	X W O	SO REC	RESULT ID Q AC Q DT 00 D
SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-THYROID, AND PARATHYROID; SCHWELZER H.J., GROSS G., MAYER H.; ADV. GENE TECHNOL. 21:228-229(1984).	RATTUS NORVEGICUS (RAT). RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. [1]	ILT 2 Q63473 Q63473; PRELIMINARY; PRT; 105 AA. Q63473; O1-NOV-1996 (TREMBLREL. O1, CREATED) O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE UPDATE) O1-JAN-1998 (TREMBLREL. O5, LAST ANNOTATION UPDATE) PARATHYROID HORMONE (FRAGMENT).	45 LRKKL 49 1 LRKKL 5	Query Match 100.0%; Score 39; DB 3; Length 65; Best Local Similarity 100.0%; Pred. No. 5.95e+01; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps	SEQUENCE FROM N.A. STRAIN-H90; MEDILINE; 94359533. FROSCH P., HARTMANN M., MUEHLSCHLEGEL F., FROSCH M.; MOL. BICCHEM. PARASITOL. 64:171-175(1994). EMBL; Z26483; G452853; NON_TER 1 1 SEQUENCE 65 AA; 7617 MW; 3F256666 CRC32;	117 1 Q24890 Q24890; Q24890; O1-NOV-1996 (TREMBLREL. O1, CREATED) O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE UPDATE) O1-NOV-1996 (TREMBLREL. O1, LAST ANNOTATION UPDATE) ANTIGEN B (FRAMENT). ECHINOCOCCUS MULTILOCULARIS. EUKARYOTA; METAZOA; ACOELOMATES; PLATYHELMINTHES; CESTODA.

0